

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 26, 2005, 08:01:20 ; Search time 127.778 Seconds  
(without alignments)  
20.038 Million cell updates/sec

Title: US-10-053-669-1  
Perfect score: 27  
Sequence: 1 FGLM 5

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum-DB-seq-length: 0  
Maximum-DB-seq-length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 150 summaries

Database :

1: Uniprot 03.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	27	100.0	11	1	TKN4_PSEGU
2	27	100.0	11	1	TKN5_PSEGU
3	27	100.0	11	1	TKNA_CAVPO
4	27	100.0	11	1	TKNA_CHICK
5	27	100.0	11	1	TKNA_HORSE
6	27	100.0	11	1	TKNA_ONCMY
7	27	100.0	11	1	TKNA_SCYCA
8	27	100.0	45	2	06L053
9	27	100.0	69	1	VATI_RHOBL
10	27	100.0	72	2	09Y454
11	27	100.0	74	2	08I1W7
12	27	100.0	76	2	086U06
13	27	100.0	82	2	06ECK5
14	27	100.0	87	2	086U07
15	27	100.0	96	2	086U08
16	27	100.0	99	2	086U09
17	27	100.0	100	2	09RD07
18	27	100.0	104	2	06ECK6
19	27	100.0	107	2	07VC12
20	27	100.0	107	2	06ECK8
21	27	100.0	108	2	08ESK7
22	27	100.0	113	2	08FW09
23	27	100.0	114	2	097947
24	27	100.0	115	2	TKN1_RABIT
25	27	100.0	116	2	09X1V2
26	27	100.0	119	2	0940P5
27	27	100.0	124	2	09CGC7
28	27	100.0	129	1	TKN1_HUMAN
29	27	100.0	130	1	TKN1_BOVIN
30	27	100.0	130	1	P01289
31	27	100.0	130	1	TKN1_MESAU

32	27	100.0	130	1	TKN1_MOUSE
33	27	100.0	130	1	TKN1_RAP
34	27	100.0	138	2	08RK61
35	27	100.0	138	2	08RK63
36	27	100.0	138	2	08RK75
37	27	100.0	147	2	09T9H7
38	27	100.0	150	2	08TMB0
39	27	100.0	150	2	053986
40	27	100.0	150	2	069CB3
41	27	100.0	150	2	069CB7
42	27	100.0	150	2	075RU4
43	27	100.0	151	2	08MBL5
44	27	100.0	151	2	08MBM2
45	27	100.0	157	2	013092
46	27	100.0	166	2	08YYS0
47	27	100.0	170	2	09TX35
48	27	100.0	170	2	07W9N5
49	27	100.0	173	2	09KAN4
50	27	100.0	179	2	08LKM8
51	27	100.0	181	2	07WME0
52	27	100.0	181	2	07MH22
53	27	100.0	208	2	07MTW2
54	27	100.0	224	2	08P1Q4
55	27	100.0	227	1	YP85_DEIRA
56	27	100.0	230	1	Y920_HELPJ
57	27	100.0	230	1	Y920_HELPJ
58	27	100.0	255	2	07WMN7
59	27	100.0	256	2	09UYK2
60	27	100.0	256	2	09K0J7
61	27	100.0	259	2	07ULC3
62	27	100.0	276	2	P72066
63	27	100.0	276	2	P72069
64	27	100.0	276	2	08R0S0
65	27	100.0	276	2	09LC64
66	27	100.0	278	2	085H03
67	27	100.0	285	2	08FY11
68	27	100.0	290	2	08SXB3
69	27	100.0	291	2	08M6V3
70	27	100.0	292	2	028568
71	27	100.0	293	2	028888
72	27	100.0	299	2	028959
73	27	100.0	299	2	029353
74	27	100.0	301	2	08YJTB6
75	27	100.0	311	2	06YJCP2
76	27	100.0	312	2	068RK4
77	27	100.0	315	2	09P967
78	27	100.0	315	2	068RK6
79	27	100.0	319	1	Y189_MYCPN
80	27	100.0	319	2	0921P8
81	27	100.0	320	2	09BSK2
82	27	100.0	321	2	08EP56
83	27	100.0	322	2	08EP56
84	27	100.0	339	2	06ER27
85	27	100.0	339	2	07MBN1
86	27	100.0	345	2	09CYJ1
87	27	100.0	355	2	08SGN7
88	27	100.0	355	2	08HDS7
89	27	100.0	355	2	08HDS7
90	27	100.0	355	2	09BSX2
91	27	100.0	355	2	09BSX3
92	27	100.0	355	2	09GBL2
93	27	100.0	355	2	09ML03
94	27	100.0	357	2	028862
95	27	100.0	375	2	09H1U3
96	27	100.0	380	2	057772
97	27	100.0	384	2	092614
98	27	100.0	389	2	087NP5
99	27	100.0	397	1	FTSN_CYAPA
100	27	100.0	402	2	021056
101	27	100.0	402	2	09NEO0
102	27	100.0	402	2	087YJ6
103	27	100.0	403	2	09XP03
104	27	100.0	403	2	09XP05

P41539	mus musculus
P06767	rattus norv
08RK61	nitrosomona
08RK63	nitrosospir
08RK75	nitrosomona
09T9H7	halocynthia
08TMB0	methanosarc
053986	nitrosomona
069CB3	uncultured
069CB7	uncultured
075RU4	uncultured
08MBL5	glytapanate
08MBM2	glytapanate
013092	homo sapien
08YYS0	anabaena sp
09TX35	disaster oc
07W9N5	borderella
09KAN4	bacillus ha
08LKM8	medicago tr
07WME0	borderella
07MH22	borderella
07MTW2	porphyromon
08P1Q4	xanthomonas
YP85_DEIRA	delnoccocus
Y920_HELPJ	helicobacte
07WMN7	helicobacte
09UYK2	neisseria m
09K0J7	neisseria m
07ULC3	rhodopirell
P72066	nitrosomona
P72069	nitrosomona
08R0S0	nitrosomona
09LC64	nitrosomona
085H03	cooperia on
08FY11	brucella su
08SXB3	drosophila
08M6V3	belenois ja
028568	archaeoglob
028888	archaeoglob
028959	archaeoglob
029353	archaeoglob
08YJTB6	brucella me
06YJCP2	schizaphis
068RK4	schlechtend
09P967	tricholoma
068RK6	diuraphis n
P75262	mycoplasma
06B42	alcaligenes
0921P8	mus musculu
09BSK2	homo sapien
08EP56	oceanobacil
06ER27	cotesia acu
07MBN1	wolinnella s
09CYJ1	mus musculu
08SGN7	carabus erw
08HDS7	carabus sit
08HDS7	carabus reg
09BSX2	ceroglossus
09BSX3	caraboglossus
09GBL2	carabus hae
09ML03	carabus art
028862	archaeoglob
09H1U3	thermoplasm
057772	pyrococcus
092614	listeria in
087NP5	vibrio para
P48280	cyamophora
021056	caenorhabdi
09NEO0	caenorhabdi
087YJ6	pseudomonas
09XP03	pholeteator
09XP05	glytapanate

105	27	100.0	403	2	Q8KLX6	Q8KLX6 pseudomonas
106	27	100.0	404	2	Q9XNZ8	Q9XNZ8 apanteles n
107	27	100.0	404	2	Q8BP27	Q8BP27 pseudomonas
108	27	100.0	407	2	Q8H139	Q8H139 arbidopsi
109	27	100.0	408	2	Q9XP01	Q9XP01 dolichogeni
110	27	100.0	408	2	Q7VX47	Q7VX47 bordetella
111	27	100.0	408	2	Q7WLE6	Q7WLE6 bordetella
112	27	100.0	409	2	Q9XP06	Q9XP06 hypomicroga
113	27	100.0	409	2	Q9XP13	Q9XP13 cotesia mar
114	27	100.0	409	2	Q9XP15	Q9XP15 apanteles c
115	27	100.0	409	2	Q6LMT6	Q6LMT6 photobacter
116	27	100.0	409	2	Q87JL6	Q87JL6 vibrio para
117	27	100.0	409	2	Q8DB26	Q8DB26 vibrio vuln
118	27	100.0	410	2	Q6EB94	Q6EB94 leiscoscyt
119	27	100.0	410	2	Q9XP00	Q9XP00 dolichogeni
120	27	100.0	410	2	Q9XP10	Q9XP10 microgaster
121	27	100.0	410	2	Q9XP11	Q9XP11 alphomelon
122	27	100.0	410	2	Q9XP14	Q9XP14 cotesia gri
123	27	100.0	411	2	Q9XNZ7	Q9XNZ7 salton falc
124	27	100.0	411	2	Q9XP04	Q9XP04 glyptapante
125	27	100.0	414	2	Q7MHX0	Q7MHX0 vibrio vuln
126	27	100.0	416	1	PUR2_CLOAB	Q97390 clostridium
127	27	100.0	419	2	Q6XV78	Q6XV78 oncorhynch
128	27	100.0	420	2	Q69F80	Q69F80 salmo salar
129	27	100.0	421	2	Q6XN52	Q6XN52 rhodococcus
130	27	100.0	425	2	Q64DQ3	Q64DQ3 uncultured
131	27	100.0	426	1	PUR2_FUSNN	Q8REV7 fusobacteri
132	27	100.0	426	2	Q7P5Q4	Q7P5Q4 fusobacteri
133	27	100.0	429	2	Q6EF43	Q6EF43 cotesia acu
134	27	100.0	434	2	Q8BL78	Q8BL78 pseudomonas
135	27	100.0	436	2	Q92NM2	Q92NM2 thizobium m
136	27	100.0	437	2	Q6BXG4	Q6BXG4 debaryomyce
137	27	100.0	439	2	P92962	P92962 arbidopsi
138	27	100.0	444	2	Q6EF44	Q6EF44 cotesia acu
139	27	100.0	440	2	Q6EF34	Q6EF34 cotesia mel
140	27	100.0	444	2	Q6EF42	Q6EF42 cotesia acu
141	27	100.0	444	2	Q6EF45	Q6EF45 cotesia acu
142	27	100.0	445	2	Q6EF21	Q6EF21 cotesia acu
143	27	100.0	445	2	Q6EF23	Q6EF23 cotesia mel
144	27	100.0	446	2	Q6EF25	Q6EF25 cotesia big
145	27	100.0	446	2	Q6EF35	Q6EF35 cotesia mel
146	27	100.0	447	2	Q6EF23	Q6EF23 cotesia big
147	27	100.0	447	2	Q6EF24	Q6EF24 cotesia big
148	27	100.0	447	2	Q6EF26	Q6EF26 cotesia big
149	27	100.0	447	2	Q6EF28	Q6EF28 cotesia mel
150	27	100.0	497	2	Q6EF29	Q6EF29 cotesia mel

## ALIGNMENTS

RESULT 1  
TKN4\_PSECU STANDARD; PRT; 11 AA.  
AC P42989;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Substance P-like peptide I (PG-SP1).  
OS Pseudophryne guentheri (Guenther's toadlet).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;  
OC Myobatrachinae; Pseudophryne.  
OX NCBI\_TaxID=30349;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Skin secretion;  
RX MEDLINE=90287814; PubMed=2356157; DOI=10.1016/0196-9781(90)90086-K;  
RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,  
RA Roberts J.D., Melchiorri P., Erspamer V.,  
RT "Six novel tachykinin- and bombesin-related peptides from the skin of  
the Australian frog Pseudophryne guentheri.",  
RL Peptides 11:299-304 (1990).

CC -1- FUNCTION: Tachykinins are active peptides which excite neurons,  
CC evoke behavioral responses, are potent vasodilators and  
CC secretagogues, and contract (directly or indirectly) many smooth  
CC muscles.  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- TISSUE SPECIFICITY: Skin.  
CC -1- SIMILARITY: Belongs to the tachykinin family.  
DR PIR; E60409; E60409.  
DR InterPro; IPR002040; Tachykinin.  
DR Pfam; PR02202; Tachykinin; 1.  
DR SMART; SM00203; TK; 1.  
DR PROSITE; PS00267; TACHYKININ; 1.  
KW Amidation; Amphibian defense peptide; Direct protein sequencing;  
KW Neuropeptide; Pyrrolidone carboxylic acid; Tachykinin.  
FT MOD\_RES 1  
FT MOD\_RES 11  
SQ SEQUENCE 11 AA; 1294 MW; 3A247C2CC9CB1A57 CRC64;

Query Match 100.0%; Score 27; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 30;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FRGLM 5  
Db 7 FRGLM 11

RESULT 2  
TKN5\_PSECU STANDARD; PRT; 11 AA.  
AC P42990;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Substance P-like peptide II (PG-SP1I).  
OS Pseudophryne guentheri (Guenther's toadlet).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;  
OC Myobatrachinae; Pseudophryne.  
OX NCBI\_TaxID=30349;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Skin secretion;  
RX MEDLINE=90287814; PubMed=2356157; DOI=10.1016/0196-9781(90)90086-K;  
RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,  
RA Roberts J.D., Melchiorri P., Erspamer V.,  
RT "Six novel tachykinin- and bombesin-related peptides from the skin of  
the Australian frog Pseudophryne guentheri.",  
RL Peptides 11:299-304 (1990).  
CC -1- FUNCTION: Tachykinins are active peptides which excite neurons,  
CC evoke behavioral responses, are potent vasodilators and  
CC secretagogues, and contract (directly or indirectly) many smooth  
CC muscles.  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- TISSUE SPECIFICITY: Skin.  
CC -1- SIMILARITY: Belongs to the tachykinin family.  
DR PIR; F60409; F60409.  
DR InterPro; IPR002040; Tachykinin.  
DR Pfam; PR02202; Tachykinin; 1.  
DR PROSITE; PS00267; TACHYKININ; 1.  
KW Amidation; Amphibian defense peptide; Direct protein sequencing;  
KW Neuropeptide; Pyrrolidone carboxylic acid; Tachykinin.  
FT MOD\_RES 1  
FT MOD\_RES 11  
SQ SEQUENCE 11 AA; 1293 MW; 3A247C2CC9CB1A57 CRC64;

Query Match 100.0%; Score 27; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 30;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FRGLM 5  
Db 7 FRGLM 11

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OM protein - protein search, using BW model

Run on: October 26, 2005, 08:04:16 ; Search time 13.333 Seconds

(without alignments)  
36.081 Million cell updates/sec

Title: US-10-053-669-1

Perfect score: 27  
Sequence: 1 FFGIM 5

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 150 summaries

Database :

PIR 79.1  
1: p1r1.\*  
2: p1r2.\*  
3: p1r3.\*  
4: p1r4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	27	100.0	11	1 A60654	substance P - guin
2	27	100.0	11	1 SPHO	substance P - hors
3	27	100.0	11	2 JN0023	substance P - chic
4	27	100.0	11	2 S33300	probable substance
5	27	100.0	11	2 E60409	substance P-like P
6	27	100.0	11	2 F60409	substance P-like P
7	27	100.0	11	2 S23308	substance P - rain
8	27	100.0	63	2 UC2412	tachykinin gamma c
9	27	100.0	69	2 S04666	hypothetical prote
10	27	100.0	72	2 JC5455	preprotachykinin-A
11	27	100.0	72	2 I62742	tachykinin A gamma
12	27	100.0	97	2 S12958	tachykinin delta p
13	27	100.0	112	1 SPRTA	substance P alpha
14	27	100.0	115	1 SPRTB	substance P gamma
15	27	100.0	115	1 SPRTG	substance P gamma
16	27	100.0	116	2 C72232	hypothetical prote
17	27	100.0	124	2 B86771	hypothetical prote
18	27	100.0	129	1 SPHUB	neurokinin 1 precu
19	27	100.0	130	1 SPBOB	neurokinin 1 precu
20	27	100.0	130	1 SPRTB	substance P beta p
21	27	100.0	130	2 S47038	tachykinin 1 precu
22	27	100.0	130	2 I52526	neurokinin 1 precu
23	27	100.0	166	2 AG1931	hypothetical prote
24	27	100.0	173	2 B83931	hypothetical prote
25	27	100.0	230	1 H64634	conserved hypotet
26	27	100.0	230	2 F71879	hypothetical prote
27	27	100.0	234	2 F75254	conserved hypotet
28	27	100.0	256	2 D81181	conserved hypotet
29	27	100.0	256	2 C81925	probable sec-indep

30	27	100.0	299	2 F69422	ISA0963-4 transpos
31	27	100.0	299	2 H69462	ISA0963-6 transpos
32	27	100.0	299	2 E69413	ISA0963-3 transpos
33	27	100.0	299	2 E69288	ISA0963-2 transpos
34	27	100.0	301	2 AE3273	transporter, dme f
35	27	100.0	319	2 S73344	probable transport
36	27	100.0	357	2 A69426	ISA0963-5 transpos
37	27	100.0	380	2 E71218	hypothetical prote
38	27	100.0	397	2 T06957	probable cell divi
39	27	100.0	416	2 A97072	phosphoribosylamin
40	27	100.0	439	2 T47713	proline transport
41	27	100.0	674	2 T20571	hypothetical prote
42	27	100.0	845	2 T25657	hypothetical prote
43	27	100.0	896	2 I45858	desmocollin - bov
44	27	100.0	1335	2 T17508	glycoprotein Vp260
45	25	92.6	79	2 AB3284	hypothetical prote
46	25	92.6	124	2 T36388	hypothetical prote
47	25	92.6	155	2 AB1545	B. subtilis ydck p
48	25	92.6	183	2 AG2944	hypothetical prote
49	25	92.6	187	2 T47342	hypothetical prote
50	25	92.6	207	2 E69124	cobalamin biosynth
51	25	92.6	207	2 C98338	hypothetical prote
52	25	92.6	258	2 A72266	hypothetical prote
53	25	92.6	266	2 A95114	hypothetical prote
54	25	92.6	266	2 B97983	secy protein homol
55	25	92.6	343	2 T01432	hypothetical prote
56	25	92.6	360	2 T27196	hypothetical prote
57	25	92.6	382	2 A70071	conserved hypotet
58	25	92.6	424	2 T44296	hypothetical prote
59	25	92.6	437	2 H81041	citrate transport
60	25	92.6	456	2 B90069	hypothetical prote
61	25	92.6	490	2 A35312	potassium channel
62	25	92.6	533	2 S62489	hypothetical prote
63	25	92.6	552	2 E69438	probable fatty-aci
64	25	92.6	553	2 T01416	secy protein homol
65	25	92.6	576	2 E86208	protein F265.12 l
66	25	92.6	659	2 AB1293	ABC transporter (p
67	25	92.6	663	2 C95153	v-type sodium ATP
68	25	92.6	664	2 B53610	ncpl protein - Ent
69	25	92.6	676	2 F69394	H+-transporting AT
70	25	92.6	776	2 S45495	isp4 protein - fis
71	25	92.6	801	2 G84370	heavy-metal transp
72	25	92.6	869	2 T32702	hypothetical prote
73	25	92.6	898	1 A44217	genome polypotein
74	25	92.6	3988	1 GNMWV	genome polypotein
75	25	88.9	10	2 B49581	salokinin II - ye
76	24	88.9	10	2 A49581	salokinin I - ye
77	24	88.9	10	2 A24867	scylliorhizin I - s
78	24	88.9	10	2 B61033	renatachynkinin B -
79	24	88.9	11	2 S07203	uperolein - frog (
80	24	88.9	11	2 S07201	physalaemin - frog
81	24	88.9	11	2 A61033	renatachynkinin A -
82	24	88.9	51	2 S34506	photosystem II pro
83	24	88.9	53	2 H82739	hypothetical prote
84	24	88.9	66	2 C42529	B-ORF-B protein -
85	24	88.9	66	2 B36855	B2L protein - vari
86	24	88.9	66	2 T28601	hypothetical prote
87	24	88.9	75	2 G69221	hypothetical prote
88	24	88.9	80	2 D97909	hypothetical prote
89	24	88.9	87	2 T22923	hypothetical prote
90	24	88.9	93	1 S2305	ribosomal protein
91	24	88.9	104	2 F72590	hypothetical prote
92	24	88.9	114	2 E72600	hypothetical prote
93	24	88.9	129	2 F70728	hypothetical prote
94	24	88.9	133	2 S27488	probable membrane
95	24	88.9	144	2 G81043	hypothetical prote
96	24	88.9	155	1 JX0226	H+-exporting ATPas
97	24	88.9	155	1 JX0263	H+-exporting ATPas
98	24	88.9	156	1 JN0456	H+-exporting ATPas
99	24	88.9	156	2 A56680	H+-exporting ATPas
100	24	88.9	159	1 S42878	H+-exporting ATPas
101	24	88.9	159	2 S32544	H+-exporting ATPas
102	24	88.9	161	2 S32970	H+-exporting ATPas

103	24	88.9	161	2	F82322	conserved hypothet
104	24	88.9	167	2	G90175	NADH dehydrogenase
105	24	88.9	169	2	D87294	ATP synthase F0, B
106	24	88.9	172	2	AE2283	hypothetical prote
107	24	88.9	178	2	JS0337	hypothetical 21k p
108	24	88.9	178	2	S07737	hypothetical prote
109	24	88.9	183	2	T44337	hypothetical prote
110	24	88.9	185	2	A64159	intracellular sept
111	24	88.9	189	2	C90592	hypothetical prote
112	24	88.9	197	2	E95011	hypothetical prote
113	24	88.9	197	2	H97882	hypothetical prote
114	24	88.9	204	2	G86304	transcription regu
115	24	88.9	206	2	C70226	hypothetical prote
116	24	88.9	215	2	UX0244	pyroglyutamyl-pepti
117	24	88.9	215	2	S23432	pyroglyutamyl-pepti
118	24	88.9	217	2	C90525	ABC transporter at
119	24	88.9	217	2	F83840	stage II sporulaci
120	24	88.9	218	2	S73626	MG364 homolog G12
121	24	88.9	219	2	D70411	hypothetical prote
122	24	88.9	220	2	AD0225	probable amino-aci
123	24	88.9	222	2	AB0750	probable ABC trans
124	24	88.9	222	2	A85809	probable transport
125	24	88.9	222	2	H90960	probable transport
126	24	88.9	222	2	C64355	probable ABC-type
127	24	88.9	224	2	C64240	mobilization prote
128	24	88.9	227	2	D86631	transposase of IS1
129	24	88.9	227	2	G86704	transposase of IS1
130	24	88.9	228	2	AE1704	hypothetical prote
131	24	88.9	228	2	AE1333	hypothetical prote
132	24	88.9	222	2	A84053	magnesium (Mg2+)-c
133	24	88.9	233	2	A87601	hypothetical prote
134	24	88.9	234	2	B64544	triosephosphate is
135	24	88.9	235	2	T24882	hypothetical prote
136	24	88.9	239	2	JC7752	F-1ANA protein - h
137	24	88.9	244	2	A69502	conserved hypothet
138	24	88.9	255	2	AG1198	conserved hypothet
139	24	88.9	255	2	AE1556	conserved hypothet
140	24	88.9	264	2	A71367	probable holocyto
141	24	88.9	264	2	T37551	hypothetical prote
142	24	88.9	265	2	A84937	undecaprenol kina
143	24	88.9	272	2	C86642	transposase of IS1
144	24	88.9	272	2	C86884	transposase of IS1
145	24	88.9	272	2	D86711	transposase of IS1
146	24	88.9	275	2	E75548	conserved hypothet
147	24	88.9	276	2	A49853	ammonia monooxygen
148	24	88.9	282	2	T19393	hypothetical prote
149	24	88.9	284	2	T33860	hypothetical prote
150	24	88.9	287	2	C84567	hypothetical prote

## ALIGNMENTS

RESULT 1  
 A60654  
 substance P - guinea pig  
 C/Species: Cavia porcellus (guinea pig)  
 C/Date: 14-May-1993 #sequence\_revision 27-Jun-1994 #text\_change 09-Jul-2004  
 C/Accession: A60654

R/Murphy, R.  
 Neuropeptides 14, 105-110, 1989  
 A/Title: Primary amino acid sequence of guinea-pig substance P.  
 A/Reference number: A60654; MUID:90044685; PMID:2478925  
 A/Accession: A60654  
 A/Molecule type: protein  
 A/Residues: 1-11 <MUR>  
 A/Cross-references: UNIPROT:P01290  
 C/Superfamily: substance P precursor  
 C/Keywords: amidated carboxyl end; neuropeptide; tachykinin  
 F/11/Modified site: amidated carboxyl end (Met) #status experimental

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 Best Local Similarity 100.0%; Pred. No. 3;

Matches	5;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
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Db	7	FFGLM 11							

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C/Species: Equus caballus (domestic horse)  
 C/Date: 23-Oct-1981 #sequence\_revision 23-Oct-1981 #text\_change 09-Jul-2004  
 C/Accession: A01558  
 R/Studer, R.O.; Tizzeclak, A.; Jergler, W.  
 Heiv. Chm. Acta 56, 860-866, 1973  
 A/Title: Isolierung und Aminosäuresequenz von Substanz P aus Pferdedarm.  
 A/Reference number: A01558  
 A/Accession: A01558  
 A/Molecule type: protein  
 A/Residues: 1-11 <STU>  
 A/Cross-references: UNIPROT:P01290  
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Qy 1  
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 Db 7  
 FFGLM 11

RESULT 3

substance P - chicken  
 C/Species: Gallus gallus (chicken)  
 C/Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 09-Jul-2004  
 C/Accession: JN0023  
 R/Conlon, J.M.; Karsoulis, S.; Schmidt, W.E.; Thim, L.  
 Regul. Pept. 20, 171-180, 1988  
 A/Title: [Arg3]substance P and neurokinin A from chicken small intestine.  
 A/Reference number: JN0023; MUID:88204263; PMID:2452461  
 A/Accession: JN0023

A/Molecule type: protein  
 A/Residues: 1-11 <CON>  
 A/Cross-references: UNIPROT:P19850  
 C/Superfamily: substance P precursor  
 C/Keywords: amidated carboxyl end; tachykinin  
 F/11/Modified site: amidated carboxyl end (Met) #status predicted

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Qy 1  
 FFGLM 5  
 Db 7  
 FFGLM 11

RESULT 4

probable substance P - smaller spotted catshark  
 C/Species: Scyliorhinus canicula (smaller spotted catshark, smaller spotted dogfish)  
 C/Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 09-Jul-2004  
 C/Accession: S33300  
 R/Waugh, D.; Wang, Y.; Hazon, N.; Balmont, R.J.; Conlon, J.M.  
 Eur. J. Biochem. 214, 469-474, 1993

A/Title: Primary structures and biological activities of substance-P-related peptides fr  
 A/Reference number: S33300; MUID:93292508; PMID:7685693  
 A/Accession: S33300  
 A/Molecule type: protein

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 26, 2005, 08:05:47 ; Search time 124.444 Seconds  
(without alignments)  
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Title: US-10-053-669-1  
Perfect score: 27  
Sequence: 1 FGLM 5

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1862994 seqs, 417510619 residues

Total number of hits satisfying chosen parameters: 1862994

Minimum DB-seq-length: 0  
Maximum DB-seq-length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 150 summaries

Database :

Published Applications AA: \*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysts of the total score distribution.

#### SUMMARIES

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2	27	100.0	5	14	US-10-053-669-1
3	27	100.0	5	15	US-10-134-187-3
4	27	100.0	5	16	US-10-688-741-3
5	27	100.0	5	17	US-10-805-881-1
6	27	100.0	5	16	US-10-720-039-3
7	27	100.0	5	17	US-10-497-628-15
8	27	100.0	5	20	US-11-066-697-604
9	27	100.0	5	20	US-11-025-494-3
10	27	100.0	6	14	US-10-168-789A-38
11	27	100.0	6	17	US-10-497-628-14

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13	27	100.0	6	20	US-11-066-697-597	Sequence 597, App
14	27	100.0	6	20	US-11-066-697-601	Sequence 601, App
15	27	100.0	7	14	US-10-036-542-110	Sequence 110, App
16	27	100.0	7	14	US-10-036-542-111	Sequence 111, App
17	27	100.0	7	14	US-10-168-789A-37	Sequence 37, App1
18	27	100.0	7	15	US-10-134-187-2	Sequence 2, App11
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; APPLICANT: Well's, Inc  
; TITLE OF INVENTION: Method for Detecting Deficient Cellular Membrane Tightly Bound Mac  
; FILE REFERENCE: 1427001  
; CURRENT APPLICATION NUMBER: US/09/265,690C  
; CURRENT FILING DATE: 1999-03-10  
; SOFTWARE: Patentin version 3.0  
; SEQ ID NO 1  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
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; NAME/KEY: MOD\_RES  
; LOCATION: (5)..(5)  
; OTHER INFORMATION: AMIDATION  
US-09-265-690C-1

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; APPLICANT: Well's, Inc  
; TITLE OF INVENTION: Method for Detecting Deficient Cellular Membrane Tightly Bound Mac  
; FILE REFERENCE: N1427-005  
; CURRENT APPLICATION NUMBER: US/10/053,669  
; CURRENT FILING DATE: 2002-01-24  
; PRIOR APPLICATION NUMBER: 09/265,690  
; PRIOR FILING DATE: 1999-03-10  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: Patentin version 3.0  
; SEQ ID NO 1  
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; TYPE: PRT  
; ORGANISM: Homo sapiens  
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; NAME/KEY: MOD\_RES  
; LOCATION: (5)..(5)  
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US-10-053-669-1

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Db 1 FFGLM 5

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US-10-134-187-3  
; Sequence 3, Application US/10134187  
; Publication No. US20030202981A1  
; GENERAL INFORMATION:  
; APPLICANT: Kream, Richard M.  
; APPLICANT: Kream, Richard M.  
; APPLICANT: Kream, Richard M.  
; TITLE OF INVENTION: Chimeric Hybrid Analgesics

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 26, 2005, 08:04:31 : Search time 33.333 Seconds  
(without alignments)  
11.197 Million cell updates/sec

Title: US-10-053-669-1  
Perfect score: 27  
Sequence: 1 PFCM 5

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 150 summaries

Database :

Issued-Parents AA: \*  
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5: /cgn2\_6/prodata/1/aa/PCTUS COMB.pep: \*  
6: /cgn2\_6/prodata/1/aa/backfile1.pep: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

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5	27	100.0	6	1 US-07-934-553-3	Sequence 3, Appl1
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7	27	100.0	6	1 US-08-430-238-15	Sequence 15, Appl1
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9	27	100.0	6	3 US-09-317-125-5	Sequence 5, Appl1
10	27	100.0	6	4 US-09-428-692-39	Sequence 39, Appl1
11	27	100.0	6	4 US-09-428-692-41	Sequence 41, Appl1
12	27	100.0	7	1 US-07-712-8288-7	Sequence 7, Appl1
13	27	100.0	7	1 US-07-737-371E-8	Sequence 8, Appl1
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17	27	100.0	9	2 US-07-737-371E-60	Sequence 60, Appl1
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87	27	100.0	12	4 US-09-922-093-5	Sequence 5, Appl1
88	27	100.0	12	4 US-09-922-093-8	Sequence 8, Appl1
89	27	100.0	12	4 US-09-403-752A-41	Sequence 41, Appl1
90	27	100.0	12	4 US-09-763-669-1	Sequence 1, Appl1
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147	27	100.0	13	4	US-09-922-098F-49	Sequence 49, Appl1
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149	27	100.0	13	4	US-09-922-098F-51	Sequence 51, Appl1
150	27	100.0	13	4	US-09-922-098F-52	Sequence 52, Appl1

## ALIGNMENTS

RESULT 1  
US-07-934-553-2  
Sequence 2, Application US/07934553  
Patent No. 5314690  
GENERAL INFORMATION:  
APPLICANT: PATTERSON, ROY  
APPLICANT: HARRIS, KATHLEEN E  
TITLE OF INVENTION: METHOD AND COMPOSITION FOR REDUCING IGE  
TITLE OF INVENTION: ANTIBODIES TO SPECIFIC ALLERGENS  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSER: TILTON, FALLON, LUNGKUS & CHESTNUT  
STREET: 100 SOUTH WACKER DRIVE  
CITY: CHICAGO  
STATE: ILLINOIS  
COUNTRY: USA  
ZIP: 60606-4002  
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/934,553  
FILING DATE: 19920821  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/705,071  
FILING DATE: 24-MAY-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: FENTRESS, SUSAN B  
REGISTRATION NUMBER: 31,327  
REFERENCE/DOCKET NUMBER: NU-9033CIP  
TELEPHONE: 312/456-8000  
TELECOMMUNICATION INFORMATION:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 amino acids  
TYPE: AMINO ACID  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-07-934-553-2  
Query Match 100.0%; Score 27; DB 1; Length 5;  
Best Local Similarity 100.0%; Pred. No. 4.1e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 FPGM 5  
Db 1 FPGM 5  
RESULT 2  
US-08-225-474-2  
Sequence 2, Application US/08225474  
Patent No. 5560915  
GENERAL INFORMATION:  
APPLICANT: PATTERSON, ROY  
APPLICANT: HARRIS, KATHLEEN E  
TITLE OF INVENTION: Method and Composition for Treating  
TITLE OF INVENTION: Ige Mediated Allergies  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSER: TILTON, FALLON, LUNGKUS & CHESTNUT  
STREET: 100 S. Wacker Drive, Suite 960  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60606-4002  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/225,474  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/934,553  
FILING DATE: 21-AUG-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/705,071  
FILING DATE: 24-MAY-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Tilton, Timothy L.  
REGISTRATION NUMBER: 16,926  
REFERENCE/DOCKET NUMBER: NU 9033-CIP2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312)-456-8000



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OM protein - protein search, using bw model

Run on: October 26, 2005, 08:00:50 ; Search time 72.222 Seconds  
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26.776 Million cell updates/sec

Title: US-10-053-669-1  
Perfect score: 27  
Sequence: 1 FGLM 5

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB-seq length: 0  
Maximum DB-seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 150 summaries

Database :

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3: geneseqp2000s:\*  
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8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
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6	27	100.0	5	2 AAR54551	Aar54551 Cholecyt
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19	27	100.0	5	7 ADF92530	Adf92530 Substance
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23	27	100.0	6	1 AAP50694	Aap50694 Sequence
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69	27	100.0	8	7 ADE94200	Ade94200 High acti
70	27	100.0	9	1 AAP50634	Aap50634 Substance
71	27	100.0	9	2 AAW92714	Aaw92714 Human tac
72	27	100.0	9	4 AAB80325	Aab80325 Human pro
73	27	100.0	9	4 AAB91446	Aab91446 Tachykini
74	27	100.0	9	4 AAB91369	Aab91369 Tachykini
75	27	100.0	9	4 AAG99348	Aag99348 Acypical
76	27	100.0	9	7 ADR92528	Adr92528 Substance
77	27	100.0	9	8 ADN95076	Adn95076 Mammalian
78	27	100.0	10	1 AAP50633	Aap50633 Substance
79	27	100.0	10	2 AAR21933	Aar21933 Substance
80	27	100.0	10	2 AAR65181	Aar65181 S. cerevi
81	27	100.0	10	2 AAY06939	Aay06939 Substance
82	27	100.0	10	2 AAW92663	Aaw92663 Human tac
83	27	100.0	10	4 AAB91445	Aab91445 Tachykini
84	27	100.0	10	4 AAG99347	Aag99347 Acypical
85	27	100.0	10	4 AAG64746	Aag64746 Substance
86	27	100.0	10	8 ADN12181	Adn12181 Amino aci
87	27	100.0	10	8 ADN27868	Adn27868 Trichomon
88	27	100.0	11	1 AAP61480	Aap61480 Sequence
89	27	100.0	11	1 AAP80332	Aap80332 Sequence
90	27	100.0	11	2 AAR11854	Aar11854 Undecapep
91	27	100.0	11	2 AAR13162	Aar13162 Sialic ac
92	27	100.0	11	2 AAR28442	Aar28442 Substance
93	27	100.0	11	2 AAR21942	Aar21942 Substance
94	27	100.0	11	2 AAR21962	Aar21962 Substance
95	27	100.0	11	2 AAR21945	Aar21945 Substance
96	27	100.0	11	2 AAR21963	Aar21963 Substance
97	27	100.0	11	2 AAR21949	Aar21949 Substance
98	27	100.0	11	2 AAR21951	Aar21951 Substance

99	27	100.0	11	2	AAR21946	Aar21946	Substance
100	27	100.0	11	2	AAR21964	Aar21964	Substance
101	27	100.0	11	2	AAR21970	Aar21970	Cyclic su
102	27	100.0	11	2	AAR21938	Aar21938	Substance
103	27	100.0	11	2	AAR21941	Aar21941	Substance
104	27	100.0	11	2	AAR21954	Aar21954	Substance
105	27	100.0	11	2	AAR22646	Aar22646	Substance
106	27	100.0	11	2	AAR85243	Aar85243	Substance
107	27	100.0	11	2	AAR77310	Aar77310	Substance
108	27	100.0	11	2	AAM33181	Aam33181	Mono-DTPA
109	27	100.0	11	2	AAM33180	Aam33180	Mono-DTPA
110	27	100.0	11	2	AAM04616	Aam04616	Substance
111	27	100.0	11	2	AAW79775	Aaw79775	Substance
112	27	100.0	11	2	AAW42973	Aaw42973	Substrate
113	27	100.0	11	2	AAW79663	Aaw79663	Substance
114	27	100.0	11	2	AAW79662	Aaw79662	Substance
115	27	100.0	11	2	AAW92679	Aaw92679	Human tac
116	27	100.0	11	2	AAW92676	Aaw92676	Human tac
117	27	100.0	11	2	AAW92720	Aaw92720	Human tac
118	27	100.0	11	2	AAW92673	Aaw92673	Human tac
119	27	100.0	11	2	AAW92708	Aaw92708	Human tac
120	27	100.0	11	2	AAW92731	Aaw92731	Human tac
121	27	100.0	11	2	AAW92670	Aaw92670	Human tac
122	27	100.0	11	2	AAW92689	Aaw92689	Human tac
123	27	100.0	11	2	AAW92715	Aaw92715	Human tac
124	27	100.0	11	2	AAW92719	Aaw92719	Human tac
125	27	100.0	11	2	AAW92680	Aaw92680	Human tac
126	27	100.0	11	2	AAW92681	Aaw92681	Human tac
127	27	100.0	11	2	AAW92672	Aaw92672	Human tac
128	27	100.0	11	2	AAW92690	Aaw92690	Human tac
129	27	100.0	11	2	AAW92685	Aaw92685	Non-cross
130	27	100.0	11	2	AAW92685	Aaw92685	Substance
131	27	100.0	11	2	AD124903	Ad124903	Substance
132	27	100.0	11	3	AAW92682	Aaw92682	Human/rat
133	27	100.0	11	3	AAW92682	Aaw92682	Cell diff
134	27	100.0	11	3	AAW92682	Aaw92682	Substance
135	27	100.0	11	3	AAW92682	Aaw92682	Peptide 1
136	27	100.0	11	3	AAW92682	Aaw92682	Peptide 1
137	27	100.0	11	4	AAW92682	Aaw92682	Previn pe
138	27	100.0	11	4	AAW92682	Aaw92682	Previn pe
139	27	100.0	11	4	AAW92682	Aaw92682	Previn pe
140	27	100.0	11	4	AAW92682	Aaw92682	Previn pe
141	27	100.0	11	4	AAW92682	Aaw92682	Previn pe
142	27	100.0	11	4	AAW92682	Aaw92682	Previn pe
143	27	100.0	11	4	AAW92682	Aaw92682	Previn pe
144	27	100.0	11	4	AAW92682	Aaw92682	Previn pe
145	27	100.0	11	4	AAW92682	Aaw92682	Previn pe
146	27	100.0	11	4	AAW92682	Aaw92682	Previn pe
147	27	100.0	11	4	AAW92682	Aaw92682	Previn pe
148	27	100.0	11	4	AAW92682	Aaw92682	Previn pe
149	27	100.0	11	4	AAW92682	Aaw92682	Previn pe
150	27	100.0	11	4	AAW92682	Aaw92682	Previn pe

ALIGNMENTS

RESULT 1  
AAR33009 standard; peptide; 5 AA.  
ID AAR33009;  
AC AAR33009;  
XX 25-MAR-2003 (revised)  
DT 02-APR-1993 (first entry)  
XX Alpha-substituted short peptide.  
DE CCK; neuropeptide; endorphin; hormone; LHRH; contraception; analgesia;  
XX improved bioavailability.  
KM Synthetic.  
XX

FH	Key	Location/Qualifiers
FT	Modified-site	4 /note= "alpha-Me-Leu"
FT	Modified-site	5 /note= "Met-NH2"
XX	MO9219254-A1.	
PN	12-NOV-1992.	
PD	15-APR-1992;	92WO-US003119.
XX	24-APR-1991;	91US-00690755.
PR	20-MAR-1992;	92US-00852086.
XX	(WARN ) WARNER LAMBERT CO.	
XX	Horwell DC, Hughes J, Richardson RS, Howson W;	
PI	WPI, 1992-398522/48.	
XX	New alpha-subst. polypeptide are e.g. selective receptor ligands - for	
PT	treating inflammation, pain, stroke, ulcers, hypertension, heart failure,	
PT	depression, cancer, asthma, psychosis, arthritis, etc.	
XX	Claim 3; Page 41; 46pp; English.	
PS	The peptide is a specifically claimed example of a group of generically	
XX	claimed mono-, di-, tri-, tetra- and penta-peptides which include a	
CC	substituent on an alpha-C atom in the chain. Such substitution may modify	
CC	the bioavailability, stability or absorbability of the peptide and hence	
CC	may improve the activity of the peptide as a drug. Depending on the	
CC	nature of the parent peptide (hormone, endorphin, CCK, NK2, chemotactic	
CC	peptide, etc.), the modified peptides are variously useful for treating	
CC	obesity, anxiety, gastrointestinal ulcers, pain, stroke, inflammation,	
CC	addictive drug withdrawal symptoms, hypertension, heart failure,	
CC	cognition or memory disorders, spasticity, depression, diabetes, cancer,	
CC	asthma, bladder dysfunction, psychosis and arthritis; and as	
CC	contraceptives. (Updated on 25-MAR-2003 to correct PN field.) (Updated on	
CC	25-MAR-2003 to correct PD field.) (Updated on 25-MAR-2003 to correct PR	
CC	field.) (Updated on 25-MAR-2003 to correct PI field.)	
XX	Sequence 5 AA;	
SQ	Query Match	100.0%; Score 27; DB 2; Length 5;
	Best Local Similarity	100.0%; Pred. No. 1.8e+06;
	Matches	5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 FRGLM 5	
DB	1 FRGLM 5	
RESULT 2		
AAR33008		
ID	AAR33008 standard; peptide; 5 AA.	
XX		
AC	AAR33008;	
XX		
XX	25-MAR-2003 (revised)	
DT	02-APR-1993 (first entry)	
XX		
XX	Alpha-substituted short peptide.	
DE		
XX	CCK; neuropeptide; endorphin; hormone; LHRH; contraception; analgesia;	
KM	improved bioavailability.	
XX		
OS	Synthetic.	
XX		
XX	Key	Location/Qualifiers
FH	Modified-site	2 /note= "alpha-Me-Phe"
FT	Modified-site	5 /note= "alpha-Me-Phe"
FT	Modified-site	5 /note= "alpha-Me-Phe"

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OM protein - protein search, using sw model

Run on: October 26, 2005, 08:12:17 ; Search time 124.444 Seconds  
(without alignments)  
20.575 Million cell updates/sec

Title: **us-10-053-669-1**  
Perfect score: 27  
Sequence: 1 FGLM 5

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 3223

Minimum DB seq length: 0  
Maximum DB seq length: 11

Post-processing: Minimum Match 0%  
Listing first 150 summaries

Database :

1: uniprot\_03.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	27	100.0	11	1	TKN4_PSEGU
2	27	100.0	11	1	TKN5_PSEGU
3	27	100.0	11	1	TKNA_CAYPO
4	27	100.0	11	1	TKNA_CHICK
5	27	100.0	11	1	TKNA_HORSE
6	27	100.0	11	1	TKNA_ONCMY
7	27	100.0	11	1	TKNA_SCYCA
8	24	88.9	10	1	TKN1_SCYCA
9	24	88.9	10	1	TKNB_RANCA
10	24	88.9	10	1	TKS1_AEDAE
11	24	88.9	10	1	TKS2_AEDAE
12	24	88.9	11	1	TKN1_UPEIN
13	24	88.9	11	1	TKN2_UPEIN
14	24	88.9	11	1	TKN2_UPEIN
15	24	88.9	11	1	TKNA_RANCA
16	24	88.9	11	1	TKNA_RANCA
17	24	88.9	11	1	TKN1_PHYRU
18	24	88.9	11	2	OSUAR8
19	21	77.8	10	1	TKNB_RANRI
20	21	77.8	10	1	TKNC_RANCA
21	21	77.8	10	1	TKN1_PHYRU
22	21	77.8	10	2	Q76ML8
23	21	77.8	11	1	TKNA_GAMMO
24	21	77.8	11	1	TKN1_ELECI
25	21	77.8	11	1	TKN1_ELEMO
26	20	74.1	10	1	TKNB_CHICK
27	20	74.1	10	1	TKNB_ONCMY
28	20	74.1	10	1	TKNK_PIG
29	20	74.1	10	1	TKNK_RANRI
30	20	74.1	10	1	TRP6_LEUMA
31	20	74.1	10	1	TRP7_LEUMA

32	20	74.1	11	1	TKN1_PSEGU	P42986 pseudophryn
33	20	74.1	11	1	TKN2_PSEGU	P42987 pseudophryn
34	20	74.1	11	1	TKN3_PSEGU	P42988 pseudophryn
35	18	66.7	9	2	O30750	O30750 erwina amy
36	18	66.7	10	1	TKU2_UREUN	P40752 urechis uni
37	18	66.7	11	2	Q9UC46	Q9UC46 homo sapien
38	17	63.0	10	1	PAP1_PARMA	P81863 pardachirus
39	17	63.0	10	2	O6JL97	O6JL97 neiseeria g
40	17	63.0	11	2	O65907	O65907 silene ajan
41	16	59.3	5	1	ALL4_CARMA	P81817 carcinus ma
42	16	59.3	7	1	ALL2_CARMA	P81805 carcinus ma
43	16	59.3	7	1	ALL3_CARMA	P81806 carcinus ma
44	16	59.3	7	1	ALL4_CARMA	P81807 carcinus ma
45	16	59.3	7	1	ALL5_CARMA	P81808 carcinus ma
46	16	59.3	7	1	ALL7_CARMA	P82158 cydia pomon
47	16	59.3	8	1	ALL2_CARMA	P81815 carcinus ma
48	16	59.3	8	1	ALL5_CARMA	P81818 carcinus ma
49	16	59.3	8	1	ALL7_CARMA	P81820 carcinus ma
50	16	59.3	8	1	ALL8_CARMA	P81821 carcinus ma
51	16	59.3	8	1	ALL9_CARMA	P82152 cydia pomon
52	16	59.3	8	1	ALL3_CARMA	P82154 cydia pomon
53	16	59.3	8	1	ALL4_CARMA	P81840 calliphora
54	16	59.3	8	1	ALL5_CARMA	P82155 cydia pomon
55	16	59.3	8	1	ALL6_CARMA	P82156 cydia pomon
56	16	59.3	8	1	ALL7_CARMA	P82157 cydia pomon
57	16	59.3	8	1	ALL8_CARMA	P81809 carcinus ma
58	16	59.3	8	1	ALL9_CARMA	P81810 carcinus ma
59	16	59.3	8	1	ALL10_CARMA	P81812 carcinus ma
60	16	59.3	9	1	ALL11_CARMA	P81813 carcinus ma
61	16	59.3	9	1	TKC1_CALVO	P81814 carcinus ma
62	16	59.3	9	1	TKC1_CALVO	P41517 calliphora
63	16	59.3	9	1	TKC1_CALVO	P16223 locusta mig
64	16	59.3	9	2	O7S3Z9	O7S3Z9 neurospora
65	16	59.3	10	1	ALL9_CARMA	P81822 carcinus ma
66	16	59.3	10	1	TKL2_LOCMI	P16224 locusta mig
67	16	59.3	10	1	TKL3_LOCMI	P30249 locusta mig
68	16	59.3	10	2	O7M3T9	O7M3T9 tritpneustes
69	16	59.3	10	2	O7M4B9	O7M4B9 heterocentr
70	16	59.3	10	2	O8GDC0	O8GDC0 escherichia
71	16	59.3	8	2	O09258	O09258 synchococc
72	15	55.6	10	2	O35013	O35013 meloidogyne
73	15	55.6	10	2	O7M278	O7M278 tritcolum tu
74	15	55.6	10	2	O52837	O52837 rhizobium 1
75	15	51.9	8	1	ALL5_CALVO	P41841 calliphora
76	14	51.9	8	2	O40530	O40530 nicotiana t
77	14	51.9	9	1	TRP4_LEUMA	P81736 leucophaea
78	14	51.9	9	2	O7M3L3	O7M3L3 penaeus van
79	14	51.9	10	2	O7SMD5	O7SMD5 homo sapien
80	14	51.9	11	2	O9R446	O9R446 neiseeria g
81	13	48.1	8	1	ALL6_CARMA	P81819 carcinus ma
82	13	48.1	8	2	O9NIX9	O9NIX9 hydrochoeru
83	13	48.1	8	2	O7M032	O7M032 ratius norv
84	13	48.1	10	1	GONI_ALLMI	P37041 alligator m
85	13	48.1	10	1	TRP8_LEUMA	P81740 leucophaea
86	13	48.1	10	2	O7M4X1	O7M4X1 basidiobolu
87	13	48.1	10	2	O9NP06	O9NP06 homo sapien
88	13	48.1	11	2	O7S183	O7S183 neurospora
89	13	48.1	11	2	O9UR55	O9UR55 pichia angu
90	13	48.1	11	2	O6U255	O6U255 litoria anu
91	13	48.1	11	2	O66X46	O66X46 oryctolagus
92	13	48.1	11	2	O6LD65	O6LD65 mus sp. hom
93	13	48.1	11	2	O7M0E2	O7M0E2 mus sp. gen
94	13	48.1	11	2	O6R205	O6R205 oncorhynch
95	12	44.4	4	1	FFKA_ATEL	P58705 anthopleura
96	12	44.4	4	1	OCP1_OCTMI	P58648 octopus min
97	12	44.4	5	1	PAP2_PARMA	P81864 pardachirus
98	12	44.4	5	1	REI1_LITRU	P82070 litoria rub
99	12	44.4	5	1	REI2_LITRU	P82071 litoria rub
100	12	44.4	5	1	REI3_LITRU	P82072 litoria rub
101	12	44.4	5	1	REI3_LITRU	P82073 litoria rub
102	12	44.4	5	1	UC22_MAIZE	P80628 zea mays (m
103	12	44.4	6	1	PAPR_MONEX	P41966 moniezia ex
104	12	44.4	8	1	CCRN_DASVI	P68125 dasyurus vl

105	12	44.4	8	1	CCKN_MACEU	Pe8126	macropus eu
106	12	44.4	8	1	DYS1_LIMIN	Pe8209	limodysnat
107	12	44.4	8	1	013591	013591	saccharomyc
108	12	44.4	8	2	09P0K3	09P0K3	homo sapien
109	12	44.4	8	2	06R408	06R408	bubalus bub
110	12	44.4	8	2	09T4Y2	09T4Y2	asterina pe
111	12	44.4	8	2	09T0D2	09T0D2	terrancos
112	12	44.4	8	2	07X139	07X139	staphylococ
113	12	44.4	8	2	07X145	07X145	staphylococ
114	12	44.4	8	2	07ZP11	07ZP11	human immun
115	12	44.4	9	1	FI8B_ERYPA	PI9346	erythrocebu
116	12	44.4	9	1	FI8B_THRGE	PI9346	theropithec
117	12	44.4	9	1	RE42_LITRU	PE8205	litorea rub
118	12	44.4	9	2	099867	099867	homo sapien
119	12	44.4	9	2	07R8U6	07R8U6	plasmodium
120	12	44.4	9	2	08MJN1	08MJN1	cebuella py
121	12	44.4	9	2	08MJN2	08MJN2	calithrix
122	12	44.4	9	2	08MJN3	08MJN3	callimico g
123	12	44.4	9	2	08MJN4	08MJN4	leontopithec
124	12	44.4	9	2	08MJN5	08MJN5	sagunus fu
125	12	44.4	9	2	08MJN6	08MJN6	actus azara
126	12	44.4	9	2	08MJN7	08MJN7	saimiri sci
127	12	44.4	9	2	08MJN8	08MJN8	cebus apell
128	12	44.4	9	2	08MJN9	08MJN9	ateles fusc
129	12	44.4	9	2	08MJT7	08MJT7	eulemur ful
130	12	44.4	9	2	08MJT8	08MJT8	eulemur ful
131	12	44.4	9	2	07M394	07M394	sus scrofa
132	12	44.4	9	2	0691D6	0691D6	anolis sagr
133	12	44.4	9	2	06XBN2	06XBN2	vicia pach
134	12	44.4	9	2	085G96	085G96	pyrrobrum
135	12	44.4	9	2	09G036	09G036	juncus efu
136	12	44.4	9	2	09MMF4	09MMF4	buteo rufin
137	12	44.4	9	2	09MMG9	09MMG9	buteo buteo
138	12	44.4	9	2	09T688	09T688	gecko gecko
139	12	44.4	9	2	PE8240	PE8240	nicotiana t
140	12	44.4	9	2	09AXH8	09AXH8	mesembryant
141	12	44.4	9	2	07M139	07M139	unidentifie
142	12	44.4	9	2	06YF34	06YF34	rattus norv
143	12	44.4	9	2	071UHO	071UHO	rattus norv
144	12	44.4	9	2	06T1E2	06T1E2	sars corona
145	12	44.4	9	2	07LZT5	07LZT5	rana escul
146	12	44.4	9	2	07ZP19	07ZP19	human immun
147	12	44.4	9	2	07ZP13	07ZP13	human immun
148	12	44.4	9	2	07ZP05	07ZP05	human immun
149	12	44.4	9	2	07ZP07	07ZP07	human immun
150	12	44.4	9	2	07ZP01	07ZP01	human immun

## ALIGNMENTS

RESULT 1  
TKN4\_PSECU STANDARD; PRT; 11 AA.  
AC P42989;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DE 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Substance P-like peptide I (PG-SP1).  
OS Pseudophryne guentheri (Guenther's toadlet).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;  
OC NCBI\_TaxID=30349;  
RN [1]  
RP TISSUE=Skin secretion;  
RX MEDLINE=90287814; PubMed=2356157; DOI=10.1016/0196-9781(90)90086-K;  
RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,  
RT Roberts J.D., Melchiorri P., Erspamer V.,  
RT "Six novel tachykinin- and bombesin-related peptides from the skin of  
the Australian frog Pseudophryne guentheri.",  
RL Peptides 11:299-304(1990).

CC - FUNCTION: Tachykinins are active peptides which excite neurons,  
CC evoke behavioral responses, are potent vasodilators and  
CC secretagogues, and contract (directly or indirectly) many smooth  
CC muscles.  
CC - SUBCELLULAR LOCATION: Secreted.  
CC - TISSUE SPECIFICITY: Skin.  
CC - SIMILARITY: Belongs to the tachykinin family.  
DR PIR; E60409; E60409. Tachy Neurokinin.  
DR InterPro; IPR002040; Tachy Neurokinin.  
DR InterPro; IPR008215; Tachykinin.  
DR Pfam; PF02202; Tachykinin; 1.  
DR SMART; SM00203; TK; 1.  
DR PROSITE; PS00267; TACHYKININ; 1.  
KW Amidation; Amphibian defense peptide; Direct protein sequencing;  
KW Neuropeptide; Pyrrolidone carboxylic acid; Tachykinin.  
FT MOD RES 1 1  
FT MOD RES 11 1  
FT MOD RES 11 1  
SQ SEQUENCE 11 AA; 1294 MW; 3A247C2CC9C81AB7 CRC64;

Query Match 100.0%; Score 27; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 30;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 FRGLM 5  
DB 7 FRGLM 11

RESULT 2  
TKN5\_PSECU STANDARD; PRT; 11 AA.  
AC P42990;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DE 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Substance P-like peptide II (PG-SP1I).  
OS Pseudophryne guentheri (Guenther's toadlet).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;  
OC NCBI\_TaxID=30349;  
RN [1]  
RP TISSUE=Skin secretion;  
RX MEDLINE=90287814; PubMed=2356157; DOI=10.1016/0196-9781(90)90086-K;  
RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,  
RT Roberts J.D., Melchiorri P., Erspamer V.,  
RT "Six novel tachykinin- and bombesin-related peptides from the skin of  
the Australian frog Pseudophryne guentheri.",  
RL Peptides 11:299-304(1990).  
CC - FUNCTION: Tachykinins are active peptides which excite neurons,  
CC evoke behavioral responses, are potent vasodilators and  
CC secretagogues, and contract (directly or indirectly) many smooth  
CC muscles.  
CC - SUBCELLULAR LOCATION: Secreted.  
CC - TISSUE SPECIFICITY: Skin.  
CC - SIMILARITY: Belongs to the tachykinin family.  
DR PIR; F60409; F60409. Tachy Neurokinin.  
DR InterPro; IPR002040; Tachy Neurokinin.  
DR Pfam; PF02202; Tachykinin; 1.  
DR PROSITE; PS00267; TACHYKININ; 1.  
KW Amidation; Amphibian defense peptide; Direct protein sequencing;  
KW Neuropeptide; Pyrrolidone carboxylic acid; Tachykinin.  
FT MOD RES 1 1  
FT MOD RES 11 1  
FT MOD RES 11 1  
SQ SEQUENCE 11 AA; 1293 MW; 3A247C2CC9C81A57 CRC64;

Query Match 100.0%; Score 27; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 30;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 FRGLM 5  
DB 7 FRGLM 11

GenCore version 5.1.6  
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OM protein - protein search, using SW model

Run on: October 26, 2005, 08:12:37 ; Search time 25.5556 Seconds  
(without alignments)  
18.825 Million cell updates/sec

Title: UG-10-053-669-1  
27  
Perfect score: 1 PFGIM 5  
Sequence:

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 1328

Minimum DB-seq-length=0  
Maximum DB seq length: 11

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 150 summaries

Database :

1: PIR 79.\*  
2: PIR1.\*  
3: PIR2.\*  
4: PIR3.\*  
5: PIR4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	27	100.0	11	1 A60654	substance P - guin
2	27	100.0	11	1 SPHO	substance P - hirs
3	27	100.0	11	1 JN0023	substance P - chic
4	27	100.0	11	2 S33300	probable substance
5	27	100.0	11	2 E60409	substance P-like P
6	27	100.0	11	2 F60409	substance P-like P
7	27	100.0	11	2 S23308	substance P - rain
8	24	88.9	10	2 B49581	substance P - rain
9	24	88.9	10	2 A49581	substance P - rain
10	24	88.9	10	2 A24867	substance P - rain
11	24	88.9	10	2 B61033	substance P - rain
12	24	88.9	11	2 S07203	substance P - rain
13	24	88.9	11	2 S07201	substance P - rain
14	24	88.9	11	2 A61033	substance P - rain
15	21	77.8	10	2 S07202	substance P - rain
16	21	77.8	10	2 C61033	substance P - rain
17	21	77.8	10	2 S27178	substance P - rain
18	21	77.8	11	1 E00CC	substance P - musky
19	21	77.8	11	1 E00CC	substance P - musky
20	21	77.8	11	1 S23306	substance P - musky
21	20	74.1	10	1 SPPGNK	substance P - musky
22	20	74.1	10	2 JN0024	substance P - musky
23	20	74.1	10	2 S23307	substance P - musky
24	20	74.1	10	2 S23307	substance P - musky
25	20	74.1	11	2 C60409	substance P - musky
26	20	74.1	11	2 C60409	substance P - musky
27	20	74.1	11	2 D60409	substance P - musky
28	18	66.7	5	2 PT0278	substance P - musky
29	18	66.7	10	2 PH0807	substance P - musky

30	17	63.0	11	2 PT0249	Ig heavy chain CRD
31	16	59.3	8	2 D47393	neuropeptide calia
32	16	59.3	10	1 ECLQ3M	tachykinin I - mig
33	16	59.3	10	1 ECLQ3M	tachykinin III - m
34	16	59.3	10	2 P60527	sperm-activating p
35	16	59.3	10	2 B60589	sperm-activating p
36	16	59.3	11	1 ECLQ2M	tachykinin II - m
37	15	55.6	7	2 E33932	Ig mu chain D regi
38	15	55.6	10	2 S06964	hypothetical prote
39	15	55.6	10	2 S19296	16k protein - poul
40	14	51.9	5	2 A44955	alkanal monooxygen
41	14	51.9	8	2 E47393	neuropeptide calia
42	14	51.9	9	2 PD0027	pev-tachykinin - p
43	13	48.1	8	2 PH1618	Ig H chain V-D-J r
44	13	48.1	8	2 PC4373	telomeric and tetr
45	13	48.1	9	2 PT0225	Ig heavy chain CDR
46	13	48.1	9	2 PH1591	Ig H chain V-D-J r
47	13	48.1	10	1 RHPG	gonadolibetin - pi
48	13	48.1	10	1 RHPG	gonadolibetin - sh
49	13	48.1	10	1 RHPG	gonadolibetin - sh
50	13	48.1	10	2 PT0230	Ig heavy chain CDR
51	13	48.1	10	2 PT0310	Ig heavy chain CDR
52	13	48.1	10	2 PH1633	Ig H chain V-D-J r
53	13	48.1	10	2 S68033	cytochrome P450 1A
54	13	48.1	10	2 A59173	nuclease Bnl (EC 3
55	13	48.1	11	2 A57458	gene Gax protein - c
56	13	48.1	11	4 PC2124	amino transferase c
57	12	44.4	4	2 J01273	neuropeptide Antho
58	12	44.4	6	2 A43129	neuropeptide GNPFR
59	12	44.4	7	1 A61324	dermorphin - Rohde
60	12	44.4	7	2 S36662	hypothetical prote
61	12	44.4	7	2 I40504	hypothetical prote
62	12	44.4	8	2 P00012	cholecystokinin -
63	12	44.4	8	2 A43001	cholecystokinin -
64	12	44.4	8	2 A42057	fibroblast growth
65	12	44.4	8	2 PH0803	T-cell receptor al
66	12	44.4	8	2 S11078	glucose-6-phosphat
67	12	44.4	8	2 T13818	cytochrome oxidase
68	12	44.4	9	2 D24180	fibronogen beta ch
69	12	44.4	9	2 F28854	fibronopeptide B -
70	12	44.4	9	2 PT0285	Ig heavy chain CRD
71	12	44.4	9	2 PT0315	Ig heavy chain CRD
72	12	44.4	9	2 PH0942	T-cell receptor be
73	12	44.4	9	2 G58502	kidney and bladder
74	12	44.4	9	2 PT0080	60K Ca binding pro
75	12	44.4	9	2 PC7074	translacion elonga
76	12	44.4	9	2 S15850	vitamin D3 26-mono
77	12	44.4	10	1 ECLQ4M	tachykinin IV - m
78	12	44.4	10	2 A13687	caeruliein-like pep
79	12	44.4	10	2 S38305	lectin GNL2 alpha
80	12	44.4	10	2 A27617	triose-phosphate i
81	12	44.4	10	2 PN0165	triose-phosphate i
82	12	44.4	10	2 A58365	neuropeptide FRFA
83	12	44.4	10	2 T13838	cytochrome-c oxida
84	12	44.4	10	2 T13976	cytochrome-c oxida
85	12	44.4	10	2 T17057	cytochrome-c oxida
86	12	44.4	10	2 T12303	cytochrome-c oxida
87	12	44.4	10	2 T14019	cytochrome-c oxida
88	12	44.4	10	2 T17060	cytochrome-c oxida
89	12	44.4	10	2 T14043	cytochrome-c oxida
90	12	44.4	10	2 T14054	cytochrome-c oxida
91	12	44.4	10	2 T17066	cytochrome-c oxida
92	12	44.4	10	2 T17069	cytochrome-c oxida
93	12	44.4	10	2 T12308	cytochrome-c oxida
94	12	44.4	10	2 T17072	cytochrome-c oxida
95	12	44.4	10	2 T12312	cytochrome-c oxida
96	12	44.4	10	2 T12316	cytochrome-c oxida
97	12	44.4	10	2 T12321	cytochrome-c oxida
98	12	44.4	10	2 T14219	cytochrome-c oxida
99	12	44.4	11	2 PT0250	Ig heavy chain CRD
100	12	44.4	11	2 S57575	T-cell receptor V-
101	12	44.4	11	2 A54348	N-acetylglucosamin
102	12	44.4	11	2 C58501	42K bile stone pro

103	12	44.4	11	2	A44755	20alpha-hydroxyste
104	12	44.4	11	2	S69349	neuropeptide Ffam1
105	11	40.7	5	2	A61445	Met-enkephalin - b
106	11	40.7	7	2	A60224	Met-enkephalin-Arg
107	11	40.7	8	2	PC4372	telomeric and tetr
108	11	40.7	9	2	E28854	fibrinopeptide B-
109	11	40.7	9	2	A11497	transaldolase (EC
110	11	40.7	9	2	D57444	neuropeptide Grb-A
111	11	40.7	9	2	D44787	calliphramide 13
112	11	40.7	9	2	D44787	bone gla protein -
113	11	40.7	10	1	GMROI2	leucosulfakinin-II
114	11	40.7	10	1	B60556	leucosulfakinin-II
115	11	40.7	11	1	GMROI	leucosulfakinin II
116	11	40.7	11	2	A40693	transgelin - sheep
117	11	40.7	11	2	A60656	perilufakinin - A
118	11	40.7	11	2	D61033	ranachykinin D -
119	11	37.0	4	2	PT0240	Ig heavy chain CRD
120	10	37.0	4	2	A53284	T-cell receptor be
121	10	37.0	5	2	G44817	27.5 kDa structura
122	10	37.0	5	2	I44817	27.5K structural p
123	10	37.0	5	2	E44817	28.5K structural p
124	10	37.0	5	2	C44817	28K structural pro
125	10	37.0	5	2	A44817	collagen alpha 1(I
126	10	37.0	6	2	B56979	T-cell receptor be
127	10	37.0	6	2	PT0643	T-cell receptor be
128	10	37.0	6	2	PT0718	T-cell receptor be
129	10	37.0	6	2	PT0589	T-cell receptor be
130	10	37.0	6	2	PT0727	Ig heavy chain CRD
131	10	37.0	7	2	PT0246	aspartate transami
132	10	37.0	7	2	A11483	T-cell receptor be
133	10	37.0	7	2	PT0663	NADH2 dehydrogenas
134	10	37.0	7	2	T09512	globulin IV alpha
135	10	37.0	7	2	S09066	T-cell receptor be
136	10	37.0	7	2	PT0529	trichodecetin II -
137	10	37.0	7	4	PC2056	protein QJ30040 -
138	10	37.0	7	4	PC2057	polygalacturonase
139	10	37.0	8	2	PA0032	Ig gamma chain C r
140	10	37.0	8	2	S13661	T-cell receptor be
141	10	37.0	8	2	PT0627	T-cell receptor be
142	10	37.0	8	2	PT0522	T-cell receptor be
143	10	37.0	8	2	PT0559	T-cell receptor be
144	10	37.0	8	2	PT0554	T-cell receptor be
145	10	37.0	8	2	PT0725	R-phycocyanin ga
146	10	37.0	8	2	A37521	sperm-activating p
147	10	37.0	8	2	A37521	sperm-activating p
148	10	37.0	8	2	E60588	sperm-activating p
149	10	37.0	8	2	E60588	sperm-activating p
150	10	37.0	8	2	G60588	sperm-activating p

## ALIGNMENTS

RESULT 1  
A60654  
Substance P - guinea pig  
C/Species: Cavia porcellus (guinea pig)  
C/Date: 14-May-1993 #sequence\_revision 27-Jun-1994 #text\_change 09-Jul-2004  
C/Accession: A60654  
R:Murphy, R.  
Neuropeptides 14, 105-110, 1989  
A/Title: Primary amino acid sequence of guinea-pig substance P.  
A/Reference number: A60654; MUID:90044685; PMID:2478925  
A/Accession: A60654  
A/Molecule type: proteoin  
A/Residues: 1-11 <MUR>  
A/Cross-references: UNIPROT:P01290  
C/Superfamily: substance P precursor  
C/Keywords: amidated carboxyl end; neuropeptide; tachykinin  
F/11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 100.0%; Score 27; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 3;

Matches	5;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
Qy	1	FFGLM 5							
Db	7	FFGLM 11							

RESULT 2  
SPHO  
Substance P - horse  
C/Species: Equus caballus (domestic horse)  
C/Date: 23-Oct-1981 #sequence\_revision 23-Oct-1981 #text\_change 09-Jul-2004  
C/Accession: A01558  
R:Studer, R.O.; Tizetciak, A.; Lergier, W.  
Helv. Chm. Acta 56, 860-866, 1973  
A/Title: Isolierung und Aminosäuresequenz von Substanz P aus Pferdedarm.  
A/Reference number: A01558  
A/Accession: A01558  
A/Molecule type: proteoin  
A/Residues: 1-11 <STU>  
A/Cross-references: UNIPROT:P01290  
C/Superfamily: substance P precursor  
C/Keywords: amidated carboxyl end; hormone  
F/11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 100.0%; Score 27; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 3;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	FFGLM 5							
Db	7	FFGLM 11							

RESULT 3  
JN0023  
Substance P - chicken  
C/Species: Gallus gallus (chicken)  
C/Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 09-Jul-2004  
C/Accession: JN0023  
R:Conlon, J.M.; Karsoulis, S.; Schmidt, W.E.; Thim, L.  
Regul. Pept. 20, 171-180, 1988  
A/Title: [Arg3]substance P and neurokinin A from chicken small intestine.  
A/Reference number: JN0023; MUID:88204263; PMID:2452461  
A/Accession: JN0023  
A/Molecule type: proteoin  
A/Residues: 1-11 <CON>  
A/Cross-references: UNIPROT:P19850  
C/Superfamily: substance P precursor  
C/Keywords: amidated carboxyl end; tachykinin  
F/11/Modified site: amidated carboxyl end (Met) #status predicted

Query Match 100.0%; Score 27; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 3;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	FFGLM 5							
Db	7	FFGLM 11							

RESULT 4  
S33300  
Probable substance P - smaller spotted catshark  
C/Species: Scyliorhinus canicula (smaller spotted catshark, smaller spotted dogfish)  
C/Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 09-Jul-2004  
C/Accession: S33300  
R:Wang, D.; Wang, Y.; Hazon, N.; Balmont, R.J.; Conlon, J.M.  
Eur. J. Biochem. 214, 469-474, 1993  
A/Title: Primary structures and biological activities of substance-P-related peptides fr  
A/Reference number: S33300; MUID:93292508; PMID:7685693  
A/Accession: S33300  
A/Molecule type: proteoin

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 26, 2005, 08:13:37 ; Search time 120.556 Seconds  
(without alignments)  
17.316 Million cell updates/sec

Title:  
Perfect score:  
Sequence:

US-10-053-669-1  
1-FCGIM-5

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched:

1862994 seqs, 417510619 residues

Total number of hits satisfying chosen parameters: 250346

Minimum DB seq length:

0

Maximum DB seq length:

11

Post-processing:

Minimum Match 0%  
Maximum Match 100%

Listing first 150 summaries

Database:

1: /pub/pdb/1apb/1apb.pdb/US07\_PUBCOMB.pep.\*  
2: /cgn2\_6/prodata/1/pubppa/US09\_NEW\_PUB.pep.\*  
3: /cgn2\_6/prodata/1/pubppa/US06\_NEW\_PUB.pep.\*  
4: /cgn2\_6/prodata/1/pubppa/US07\_NEW\_PUB.pep.\*  
5: /cgn2\_6/prodata/1/pubppa/US06\_PUBCOMB.pep.\*  
6: /cgn2\_6/prodata/1/pubppa/US08\_NEW\_PUB.pep.\*  
7: /cgn2\_6/prodata/1/pubppa/US08\_NEW\_PUB.pep.\*  
8: /cgn2\_6/prodata/1/pubppa/US09\_PUBCOMB.pep.\*  
9: /cgn2\_6/prodata/1/pubppa/US09\_PUBCOMB.pep.\*  
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12: /cgn2\_6/prodata/1/pubppa/US09\_NEW\_PUB.pep.\*  
13: /cgn2\_6/prodata/1/pubppa/US10\_PUBCOMB.pep.\*  
14: /cgn2\_6/prodata/1/pubppa/US10\_PUBCOMB.pep.\*  
15: /cgn2\_6/prodata/1/pubppa/US10\_PUBCOMB.pep.\*  
16: /cgn2\_6/prodata/1/pubppa/US10\_PUBCOMB.pep.\*  
17: /cgn2\_6/prodata/1/pubppa/US10\_PUBCOMB.pep.\*  
18: /cgn2\_6/prodata/1/pubppa/US10\_NEW\_PUB.pep.\*  
19: /cgn2\_6/prodata/1/pubppa/US11\_PUBCOMB.pep.\*  
20: /cgn2\_6/prodata/1/pubppa/US11\_NEW\_PUB.pep.\*  
21: /cgn2\_6/prodata/1/pubppa/US60\_NEW\_PUB.pep.\*  
22: /cgn2\_6/prodata/1/pubppa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Length	ID	Description
1	27	100.0	5 9 US-09-265-690C-1	Sequence 1, App1
2	27	100.0	5 14 US-10-053-669-1	Sequence 1, App1
3	27	100.0	5 15 US-10-134-187-3	Sequence 3, App1
4	27	100.0	5 16 US-10-688-741-3	Sequence 3, App1
5	27	100.0	5 16 US-10-805-881-1	Sequence 3, App1
6	27	100.0	5 16 US-10-720-039-3	Sequence 3, App1
7	27	100.0	5 17 US-10-497-628-15	Sequence 15, App1
8	27	100.0	5 20 US-11-066-697-604	Sequence 604, App
9	27	100.0	5 20 US-11-025-494-3	Sequence 38, App1
10	27	100.0	6 14 US-10-168-789A-38	Sequence 38, App1
11	27	100.0	6 17 US-10-497-628-14	Sequence 14, App1

12	27	100.0	6 20 US-11-066-697-595	Sequence 595, App
13	27	100.0	6 20 US-11-066-697-597	Sequence 597, App
14	27	100.0	6 20 US-11-066-697-601	Sequence 601, App
15	27	100.0	7 14 US-10-036-542-110	Sequence 110, App
16	27	100.0	7 14 US-10-036-542-111	Sequence 111, App
17	27	100.0	7 14 US-10-168-789A-37	Sequence 37, App1
18	27	100.0	7 15 US-10-134-187-2	Sequence 2, App1
19	27	100.0	7 16 US-10-688-741-2	Sequence 2, App1
20	27	100.0	7 16 US-10-720-039-2	Sequence 2, App1
21	27	100.0	7 17 US-10-497-628-13	Sequence 13, App1
22	27	100.0	7 20 US-11-066-697-596	Sequence 596, App
23	27	100.0	7 20 US-11-066-697-607	Sequence 607, App
24	27	100.0	7 20 US-11-025-494-2	Sequence 2, App1
25	27	100.0	8 14 US-10-168-789A-36	Sequence 36, App1
26	27	100.0	8 17 US-10-497-628-12	Sequence 12, App1
27	27	100.0	8 20 US-11-066-697-583	Sequence 583, App
28	27	100.0	8 20 US-11-066-697-582	Sequence 582, App
29	27	100.0	8 20 US-11-066-697-600	Sequence 600, App
30	27	100.0	9 14 US-10-036-542-112	Sequence 112, App
31	27	100.0	9 14 US-10-168-789A-35	Sequence 35, App1
32	27	100.0	9 15 US-10-134-187-1	Sequence 1, App1
33	27	100.0	9 16 US-10-688-741-1	Sequence 1, App1
34	27	100.0	9 16 US-10-720-039-1	Sequence 1, App1
35	27	100.0	9 20 US-11-066-697-545	Sequence 545, App
36	27	100.0	9 20 US-11-066-697-622	Sequence 622, App
37	27	100.0	9 20 US-11-025-494-1	Sequence 1, App1
38	27	100.0	10 14 US-10-168-789A-34	Sequence 34, App1
39	27	100.0	10 17 US-10-451-304-1	Sequence 1, App1
40	27	100.0	10 20 US-11-066-697-621	Sequence 621, App
41	27	100.0	10 20 US-11-079-147-71	Sequence 71, App
42	27	100.0	11 9 US-09-265-690C-3	Sequence 3, App1
43	27	100.0	11 9 US-09-335-682-64	Sequence 64, App1
44	27	100.0	11 9 US-09-841-0918-26	Sequence 26, App1
45	27	100.0	11 10 US-09-988-792-1	Sequence 1, App1
46	27	100.0	11 10 US-09-988-792-6	Sequence 6, App1
47	27	100.0	11 10 US-09-988-792-7	Sequence 7, App1
48	27	100.0	11 10 US-09-988-792-8	Sequence 8, App1
49	27	100.0	11 13 US-09-988-792-10	Sequence 10, App1
50	27	100.0	11 13 US-10-002-593-4	Sequence 4, App1
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150 21 77.8 5 16 US-10-346-737A-30 Sequence 30, Appl
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## ALIGNMENTS

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; Publication No. US20010051345A1
; GENERAL INFORMATION:
; APPLICANT: Well's, Ibert
; TITLE OF INVENTION: Method for Detecting Deficient Cellular Membrane Tightly Bound Mac
; FILE REFERENCE: 1427001
; CURRENT APPLICATION NUMBER: US/09/265,690C
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (5)..(5)
; OTHER INFORMATION: AMIDATION
US-09-265-690C-1
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Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 FFGLM 5
Db 1 FFGLM 5
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; Publication No. US20030077658A1
; GENERAL INFORMATION:
; APPLICANT: Well's, Ibert
; TITLE OF INVENTION: Method for Detecting Deficient Cellular Membrane Tightly Bound Mac
; FILE REFERENCE: N1427-005
; CURRENT APPLICATION NUMBER: US/10/053,669
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 09/265,690
; PRIOR FILING DATE: 1999-03-10
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (5)..(5)
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US-10-053-669-1
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Query Match 100.0%; Score 27; DB 14; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 FFGLM 5
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; Sequence 3, Application US/10134187
; Publication No. US20030202981A1
; GENERAL INFORMATION:
; APPLICANT: Kreem, Richard M.
; APPLICANT: Kreem, Richard M.
; APPLICANT: Kreem, Richard M.
; TITLE OF INVENTION: Chimeric Hybrid Analgesics
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

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Title: US-10-053-669-1  
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Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 125705

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%

Listing first 150 summaries

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

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## ALIGNMENTS

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US-07-934-553-2  
Sequence 2, Application US/07934553  
Patent No. 5314690  
GENERAL INFORMATION:  
APPLICANT: PATTERSON, ROY  
APPLICANT: HARRIS, KATHLEEN E  
TITLE OF INVENTION: METHOD AND COMPOSITION FOR REDUCING IGE  
TITLE OF INVENTION: ANTIBODIES TO SPECIFIC ALLERGENS  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: TILTON, FALLON, LUNGUMUS & CHESTNUT  
STREET: 100 SOUTH WACKER DRIVE  
CITY: CHICAGO  
STATE: ILLINOIS  
COUNTRY: USA  
ZIP: 60606-4002  
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/934,553  
FILING DATE: 19920821  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/705,071  
FILING DATE: 24-MAY-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: FENTRESS, SUSAN B  
REGISTRATION NUMBER: 31,327  
REFERENCE/DOCKET NUMBER: NU-9033CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/456-8000  
INFORMATION FOR SEQ. ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 amino acids  
TYPE: AMINO ACID  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-07-934-553-2

Query Match 100.0%; Score 27; DB 1; Length 5;  
Best Local Similarity 100.0%; Pred. No. 4.1e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PFGLM 5  
Db 1 PFGLM 5

RESULT 2  
US-08-225-474-2  
Sequence 2, Application US/08225474  
Patent No. 5560915  
GENERAL INFORMATION:  
APPLICANT: Patterson, Roy  
APPLICANT: Harris, Kathleen E  
TITLE OF INVENTION: Method and Composition for Treating  
TITLE OF INVENTION: Ige Mediated Allergies  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Tilton, Fallon, Lungmus & Chestnut  
STREET: 100 S. Wacker Drive, Suite 960  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60606-4002  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/225,474  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/934,553  
FILING DATE: 21-AUG-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/705,071  
FILING DATE: 24-MAY-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Tilton, Timothy L.  
REGISTRATION NUMBER: 16,926  
REFERENCE/DOCKET NUMBER: NU 9033-CIP2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312)-456-8000

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 26, 2005, 08:08:06 ; Search time 133.333 Seconds  
(without alignments)  
14,504 Million cell updates/sec

Title: GUSEM003086699-1  
Perfect score: 27  
Sequence: 1 FGLM 5

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 494136

Minimum DB seq length: 0  
Maximum DB seq length: 11

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 150 summaries

Database : A\_Geneseq\_16Dec04:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	27	100.0	5	2 AAR33009	Aar33009 Alpha-sub
2	27	100.0	5	2 AAR33008	Aar33008 Alpha-sub
3	27	100.0	5	2 AAR33007	Aar33007 Alpha-sub
4	27	100.0	5	2 AAR33010	Aar33010 Alpha-sub
5	27	100.0	5	2 AAR54549	Aar54549 Cholecyt
6	27	100.0	5	2 AAR54551	Aar54551 Cholecyt
7	27	100.0	5	2 AAR54550	Aar54550 Cholecyt
8	27	100.0	5	2 AAR54548	Aar54548 Cholecyt
9	27	100.0	5	2 AAR41687	Aar41687 Tetrapt
10	27	100.0	5	2 AAR99643	Aar99643 Substance
11	27	100.0	5	2 AAY50325	Aay50325 Neutroph
12	27	100.0	5	2 AAW92660	Aaw92660 Human tac
13	27	100.0	5	3 AAB23025	Aab23025 Human/rat
14	27	100.0	5	3 AAY67576	Aay67576 P antigen
15	27	100.0	5	4 AAB91428	Aab91428 Tachykin
16	27	100.0	5	5 ABB10088	Abb10088 Substance
17	27	100.0	5	5 AAU77845	Aau77845 Tachykin
18	27	100.0	5	7 ADE94203	Ade94203 High acti
19	27	100.0	5	8 ADF92530	Adf92530 Mammalian
20	27	100.0	5	8 ADN95078	Adn95078 Mammalian
21	27	100.0	5	8 ADR43771	Aadr43771 Human mag
22	27	100.0	6	1 AAP40519	Aap40519 Sequence
23	27	100.0	6	1 AAP50694	Aap50694 Substance
24	27	100.0	6	1 AAP50632	Aap50632 Substance
25	27	100.0	6	1 AAP61486	Aap61486 Peptide h

26	27	100.0	6	2 AAR07893	Aar07893 Cyllopept
27	27	100.0	6	2 AAR21959	Aar21959 Substance
28	27	100.0	6	2 AAR27694	Aar27694 Cyclic ta
29	27	100.0	6	2 AAW9686	Aaw9686 Substance
30	27	100.0	6	2 AAW92706	Aaw92706 Human tac
31	27	100.0	6	2 AAW92659	Aaw92659 Human tac
32	27	100.0	6	3 AAY67575	Aay67575 P antigen
33	27	100.0	6	4 AAB82453	Aab82453 Fluorinat
34	27	100.0	6	4 AAB82436	Aab82436 Fluorinat
35	27	100.0	6	4 AAB91421	Aab91421 Tachykin
36	27	100.0	6	4 AAB91425	Aab91425 Tachykin
37	27	100.0	6	4 AAB91419	Aab91419 Tachykin
38	27	100.0	6	4 AAG99351	Aag99351 Acypical
39	27	100.0	6	4 AAB98884	Aab98884 Chimeric
40	27	100.0	6	4 AAB98886	Aab98886 Chimeric
41	27	100.0	6	5 ABB10086	Abb10086 Substance
42	27	100.0	6	7 ADE94202	Ade94202 High acti
43	27	100.0	7	2 AAR21956	Aar21956 Substance
44	27	100.0	7	2 AAR21957	Aar21957 Substance
45	27	100.0	7	2 AAY50324	Aay50324 Neutroph
46	27	100.0	7	2 AAW92662	Aaw92662 Human tac
47	27	100.0	7	2 AAW92705	Aaw92705 Human tac
48	27	100.0	7	3 AAY67574	Aay67574 P antigen
49	27	100.0	7	4 AAB80323	Aab80323 Human pro
50	27	100.0	7	4 AAB80324	Aab80324 Human pro
51	27	100.0	7	4 AAB91431	Aab91431 Tachykin
52	27	100.0	7	4 AAB91420	Aab91420 Tachykin
53	27	100.0	7	4 AAG99350	Aag99350 Acypical
54	27	100.0	7	4 AAB98845	Aab98845 Chimeric
55	27	100.0	7	5 ABB09500	Abb09500 Substance
56	27	100.0	7	7 ADE94201	Ade94201 High acti
57	27	100.0	7	7 ADF92529	Adf92529 Substance
58	27	100.0	7	8 ADN95077	Adn95077 Mammalian
59	27	100.0	8	1 AAP20303	Aap20303 Gastroint
60	27	100.0	8	2 AAR28444	Aar28444 Neurokin
61	27	100.0	8	2 AAW92664	Aaw92664 Human tac
62	27	100.0	8	2 AAW92710	Aaw92710 Human tac
63	27	100.0	8	3 AAY67573	Aay67573 P antigen
64	27	100.0	8	4 AAB91407	Aab91407 Tachykin
65	27	100.0	8	4 AAB91416	Aab91416 Tachykin
66	27	100.0	8	4 AAB91424	Aab91424 Tachykin
67	27	100.0	8	4 AAG99349	Aag99349 Acypical
68	27	100.0	8	5 ABB09498	Abb09498 Substance
69	27	100.0	8	7 ADE94200	Ade94200 High acti
70	27	100.0	9	1 AAP50634	Aap50634 Substance
71	27	100.0	9	2 AAW92714	Aaw92714 Human tac
72	27	100.0	9	4 AAB80325	Aab80325 Human pro
73	27	100.0	9	4 AAB91446	Aab91446 Tachykin
74	27	100.0	9	4 AAB91369	Aab91369 Tachykin
75	27	100.0	9	4 AAG99348	Aag99348 Acypical
76	27	100.0	9	7 ADF92528	Adf92528 Substance
77	27	100.0	9	8 ADN95076	Adn95076 Mammalian
78	27	100.0	10	1 AAP50633	Aap50633 Substance
79	27	100.0	10	2 AAR21933	Aar21933 Substance
80	27	100.0	10	2 AAR65181	Aar65181 S. cerevi
81	27	100.0	10	2 AAY06939	Aay06939 Substance
82	27	100.0	10	2 AAW92663	Aaw92663 Human tac
83	27	100.0	10	4 AAB91445	Aab91445 Tachykin
84	27	100.0	10	4 AAG99347	Aag99347 Acypical
85	27	100.0	10	4 AAG64746	Aag64746 Substance
86	27	100.0	10	8 ADN12181	Adn12181 Amino aci
87	27	100.0	10	8 ADN27868	Adn27868 Trichomon
88	27	100.0	11	1 AAP61480	Aap61480 Sequence
89	27	100.0	11	1 AAP80312	Aap80312 Sequence
90	27	100.0	11	2 AAR11854	Aar11854 Undecapep
91	27	100.0	11	2 AAR13162	Aar13162 Sialic ac
92	27	100.0	11	2 AAR28442	Aar28442 Substance
93	27	100.0	11	2 AAR21942	Aar21942 Substance
94	27	100.0	11	2 AAR21962	Aar21962 Substance
95	27	100.0	11	2 AAR21945	Aar21945 Substance
96	27	100.0	11	2 AAR21963	Aar21963 Substance
97	27	100.0	11	2 AAR21949	Aar21949 Substance
98	27	100.0	11	2 AAR21951	Aar21951 Substance

99	27	100.0	11	2	AAR21946	Aar21946	Substance
100	27	100.0	11	2	AAR21964	Aar21964	Substance
101	27	100.0	11	2	AAR21970	Aar21970	Cyclic su
102	27	100.0	11	2	AAR21938	Aar21938	Substance
103	27	100.0	11	2	AAR21941	Aar21941	Substance
104	27	100.0	11	2	AAR21954	Aar21954	Substance
105	27	100.0	11	2	AAR42646	Aar42646	Neurokinin
106	27	100.0	11	2	AAR85243	Aar85243	Substance
107	27	100.0	11	2	AAR77310	Aar77310	Substance
108	27	100.0	11	2	AAW3181	AAw3181	Mono-DTPA
109	27	100.0	11	2	AAW3180	AAw3180	Mono-DTPA
110	27	100.0	11	2	AAW04616	AAw04616	Substance
111	27	100.0	11	2	AAW79775	AAw79775	Substance
112	27	100.0	11	2	AAW42973	AAw42973	Substrate
113	27	100.0	11	2	AAW79663	AAw79663	Substrate
114	27	100.0	11	2	AAW79662	AAw79662	Substance
115	27	100.0	11	2	AAW92679	AAw92679	Human tac
116	27	100.0	11	2	AAW92675	AAw92675	Human tac
117	27	100.0	11	2	AAW92720	AAw92720	Human tac
118	27	100.0	11	2	AAW92673	AAw92673	Human tac
119	27	100.0	11	2	AAW92708	AAw92708	Human tac
120	27	100.0	11	2	AAW92731	AAw92731	Human tac
121	27	100.0	11	2	AAW92670	AAw92670	Human tac
122	27	100.0	11	2	AAW92689	AAw92689	Human tac
123	27	100.0	11	2	AAW92715	AAw92715	Human tac
124	27	100.0	11	2	AAW92719	AAw92719	Human tac
125	27	100.0	11	2	AAW92680	AAw92680	Human tac
126	27	100.0	11	2	AAW92681	AAw92681	Human tac
127	27	100.0	11	2	AAW92672	AAw92672	Human tac
128	27	100.0	11	2	AAW92690	AAw92690	Human tac
129	27	100.0	11	2	AAW30985	AAw30985	Non-cross
130	27	100.0	11	2	AAW03156	AAw03156	Substance
131	27	100.0	11	2	AD124903	AD124903	Substance
132	27	100.0	11	3	AAW23027	AAw23027	Human/rat
133	27	100.0	11	3	AAW18483	AAw18483	Peptide s
134	27	100.0	11	3	AAW32382	AAw32382	Cell diff
135	27	100.0	11	3	AAW06260	AAw06260	Substance
136	27	100.0	11	3	AAW08614	AAw08614	Peptide 1
137	27	100.0	11	4	AAW50311	AAw50311	Previn pe
138	27	100.0	11	4	AAW50312	AAw50312	Previn pe
139	27	100.0	11	4	AAW50306	AAw50306	Substance
140	27	100.0	11	4	AAW50316	AAw50316	Previn pe
141	27	100.0	11	4	AAW50544	AAw50544	Prolyl en
142	27	100.0	11	4	AAW91450	AAw91450	Tachykin
143	27	100.0	11	4	AAW91438	AAw91438	Tachykin
144	27	100.0	11	4	AAW91449	AAw91449	Tachykin
145	27	100.0	11	4	AAW91402	AAw91402	Tachykin
146	27	100.0	11	4	AAW91436	AAw91436	Tachykin
147	27	100.0	11	4	AAW93358	AAw93358	ATT-short
148	27	100.0	11	4	AAW93354	AAw93354	Substance
149	27	100.0	11	4	AAW93337	AAw93337	Human aty
150	27	100.0	11	4	AAU07298	AAu07298	Substance

## ALIGNMENTS

## RESULT 1

AAW33009  
ID AAR33009 standard; peptide; 5 AA.

AC AAR33009;

DT 25-MAR-2003 (revised)

DT 02-APR-1993 (first entry)

XX Alpha-substituted short peptide.

XX CCK; neuropeptide; endorphin; hormone; LHRH; contraception; analgesia;

XX improved bioavailability.

XX Synthetic.

XX

PH	Key	Location/Qualifiers
FT	Modified-site	4 /note= "alpha-Me-Leu"
FT	Modified-site	5 /note= "Met-NH2"
XX	WO9219254-A1.	
XX	12-NOV-1992.	
XX	15-APR-1992;	92WO-US003119.
XX	24-APR-1991;	91US-00690755.
XX	20-MAR-1992;	92US-00852086.
XX	(WARN ) WARNER LAMBERT CO.	
PI	Horwell DC, Hughes J, Richardson RS, Howson W;	
XX	WPI; 1992-398522/48.	
XX	New alpha-subst. polypeptide are e.g. selective receptor ligands - for	
PT	treating inflammation, pain, stroke, ulcers, hypertension, heart failure,	
PT	depression, cancer, asthma, psychosis, arthritis, etc.	
XX	Claim 3; Page 41; 46pp; English.	
PS	The peptide is a specifically claimed example of a group of generically	
CC	claimed mono-, di-, tri-, tetra- and penta-peptides which include a	
CC	substituent on an alpha-C atom in the chain. Such substitution may modify	
CC	the bioavailability, stability or absorbability of the peptide and hence	
CC	may improve the activity of the peptide as a drug. Depending on the	
CC	nature of the parent peptide (hormone, endorphin, CCK, NK2, chemotactic	
CC	peptide, etc.), the modified peptides are variously useful for treating	
CC	obesity, anxiety, gastrointestinal ulcers, pain, stroke, inflammation,	
CC	addictive drug withdrawal symptoms, hypertension, heart failure,	
CC	cognition or memory disorders, spasticity, depression, diabetes, cancer,	
CC	asthma, bladder dysfunction, psychosis and arthritis; and as	
CC	contraceptives. (Updated on 25-MAR-2003 to correct PN field.) (Updated on	
CC	25-MAR-2003 to correct PD field.) (Updated on 25-MAR-2003 to correct PR	
CC	field.) (Updated on 25-MAR-2003 to correct PI field.)	
XX	Sequence 5 AA;	
SO	Query Match	100.0%; Score 27; DB 2; Length 5;
	Best Local Similarity	100.0%; Pred. No. 1.8e+06;
	Matches	5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FFGLM 5  
Db 1 FFGLM 5

## RESULT 2

AAW33008  
ID AAR33008 standard; peptide; 5 AA.

AC AAR33008;

DT 25-MAR-2003 (revised)

DT 02-APR-1993 (first entry)

XX Alpha-substituted short peptide.

XX CCK; neuropeptide; endorphin; hormone; LHRH; contraception; analgesia;

XX improved bioavailability.

XX Synthetic.

XX

FT Key 2 Location/Qualifiers

FT Modified-site /note= "alpha-Me-Phe"

FT Modified-site 5

GenCore version 5.1.6  
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OM protein - protein search, using SW model

Run on: October 26, 2005, 08:01:20 ; Search time 102.222 Seconds  
(without alignments)  
20.038 Million cell updates/sec

Title: US-10-053-669-2  
Perfect score: 21  
Sequence: 1 FGLM 4

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB-seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 150 summaries

Database : uniprot\_03.\*  
1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	21	100.0	11	1	TKN4_PSEBU
2	21	100.0	11	1	TKN5_PSEBU
3	21	100.0	11	1	TKNA_CAVPO
4	21	100.0	11	1	TKNA_CHICK
5	21	100.0	11	1	TKNA_HORSE
6	21	100.0	11	1	TKNA_ONCMY
7	21	100.0	11	1	TKNA_SCYCA
8	21	100.0	19	2	PA2S_HUMAN
9	21	100.0	19	2	Q9SBE2
10	21	100.0	41	2	Q7UFW5
11	21	100.0	45	2	Q6LD93
12	21	100.0	46	2	Q87RM6
13	21	100.0	53	2	Q9TY14
14	21	100.0	55	2	O17544
15	21	100.0	55	2	O44360
16	21	100.0	56	1	YRZK_BACSU
17	21	100.0	58	2	Q8EMW4
18	21	100.0	63	2	Q6R1A0
19	21	100.0	63	2	Q9GML1
20	21	100.0	63	2	Q6ZBO3
21	21	100.0	63	2	Q82X04
22	21	100.0	64	2	Q86H30
23	21	100.0	67	2	Q8TLY1
24	21	100.0	67	2	Q8GTG4
25	21	100.0	68	2	Q05625
26	21	100.0	68	2	Q50886
27	21	100.0	69	1	Y010_TROM8
28	21	100.0	69	1	Y010_TROM8
29	21	100.0	69	1	YAT1_RHOBL
30	21	100.0	72	2	Q9Y494
31	21	100.0	72	2	Q9GP92

32	21	100.0	72	2	Q8CSF7	Q8CSF7 staphylococ
33	21	100.0	74	2	Q81W27	Q81W27 homo sapien
34	21	100.0	76	2	Q86U06	Q86U06 homo sapien
35	21	100.0	78	2	Q8VW82	Q8VW82 colwellia m
36	21	100.0	78	2	Q8UK03	Q8UK03 agrobacteri
37	21	100.0	79	2	Q8HN49	Q8HN49 brugia mala
38	21	100.0	79	2	Q8K214	Q8K214 uncultured
39	21	100.0	80	2	Q47577	Q47577 onchocerca
40	21	100.0	80	2	Q98N11	Q98N11 rhizobium 1
41	21	100.0	81	2	Q8XN79	Q8XN79 clostridium
42	21	100.0	81	2	Q7MD50	Q7MD50 vibrio vuln
43	21	100.0	81	2	Q8D627	Q8D627 vibrio vuln
44	21	100.0	82	2	Q6ECS7	Q6ECS7 oryctolagus
45	21	100.0	83	2	Q6TRW3	Q6TRW3 sulfolobus
46	21	100.0	84	2	Q6TMR5	Q6TMR5 aryaia de
47	21	100.0	84	2	Q6YMP7	Q6YMP7 aryaia de
48	21	100.0	84	2	Q8B405	Q8B405 streptococ
49	21	100.0	84	2	Q99927	Q99927 carnation m
50	21	100.0	84	2	Q683S5	Q683S5 carnation m
51	21	100.0	85	2	Q26173	Q26173 methanobact
52	21	100.0	87	2	Q86U07	Q86U07 homo sapien
53	21	100.0	88	2	Q8L778	Q8L778 vibriophaga
54	21	100.0	88	2	Q7UCH0	Q7UCH0 rhodospirill
55	21	100.0	89	2	Q49761	Q49761 mycobacteri
56	21	100.0	90	1	Y040_CORGL	Y040_CORGL
57	21	100.0	90	1	YF1M_ECOLI	YF1M_ECOLI
58	21	100.0	90	2	Q8H9X0	Q8H9X0 pseudomonas
59	21	100.0	90	2	Q94JMG	Q94JMG oryza sativ
60	21	100.0	90	2	Q7UBW7	Q7UBW7 shigella fl
61	21	100.0	90	2	Q8X9F4	Q8X9F4 escherichia
62	21	100.0	93	2	Q658H4	Q658H4 oryza sativ
63	21	100.0	93	2	Q92916	Q92916 escherichia
64	21	100.0	95	1	MG8B_HUMAN	MG8B_HUMAN
65	21	100.0	96	1	Y87A_HAELN	Y87A_HAELN
66	21	100.0	96	2	Q6M0E2	Q6M0E2 methanococ
67	21	100.0	96	2	Q86U08	Q86U08 homo sapien
68	21	100.0	97	2	Q68974	Q68974 synechococ
69	21	100.0	97	2	Q920K2	Q920K2 cavia porce
70	21	100.0	99	2	Q9RD07	Q9RD07 streptomyce
71	21	100.0	100	2	Q6ECK6	Q6ECK6 cryotolagus
72	21	100.0	100	2	Q63W33	Q63W33 burkholderi
73	21	100.0	102	2	Q9Y657	Q9Y657 aeropyrum p
74	21	100.0	104	2	Q6SGW8	Q6SGW8 uncultured
75	21	100.0	104	2	Q92M66	Q92M66 rhizobium m
76	21	100.0	104	2	Q7VC12	Q7VC12 prochloroxo
77	21	100.0	105	2	Q9YC76	Q9YC76 aeropyrum p
78	21	100.0	106	2	Q9PMK7	Q9PMK7 campylobact
79	21	100.0	107	2	Q6ECK8	Q6ECK8 homo sapien
80	21	100.0	107	2	Q7X2C5	Q7X2C5 rhodocyclis
81	21	100.0	107	2	Q6NBV3	Q6NBV3 rhodopseudo
82	21	100.0	107	2	Q8E527	Q8E527 streptococ
83	21	100.0	108	2	Q8FWT0	Q8FWT0 brucella su
84	21	100.0	109	2	Q16164	Q16164 homo sapien
85	21	100.0	109	2	Q9G049	Q9G049 phage phi11h
86	21	100.0	109	2	Q8H7P1	Q8H7P1 oryza sativ
87	21	100.0	109	2	Q6SK09	Q6SK09 bacillus th
88	21	100.0	109	2	Q81X85	Q81X85 bacillus an
89	21	100.0	110	1	COX4_BACSU	COX4_BACSU
90	21	100.0	111	2	Q6M195	Q6M195 methanococ
91	21	100.0	112	2	Q9XES4	Q9XES4 arabidopsis
92	21	100.0	113	2	Q86U09	Q86U09 homo sapien
93	21	100.0	113	2	Q7NH21	Q7NH21 gloeobacter
94	21	100.0	114	1	YE96_METUA	YE96_METUA
95	21	100.0	114	2	Q97947	Q97947 cupatia glis
96	21	100.0	114	2	Q83K17	Q83K17 shigella fl
97	21	100.0	114	2	Q8FP03	Q8FP03 escherichia
98	21	100.0	115	1	TKN1_RABIT	TKN1_RABIT
99	21	100.0	115	2	Q920K1	Q920K1 oryctolagus
100	21	100.0	115	2	Q920K1	Q920K1 vibrio angu
101	21	100.0	116	2	Q6YU06	Q6YU06 cavia porce
102	21	100.0	116	2	Q9HXG9	Q9HXG9 pseudomonas
103	21	100.0	116	2	Q9X1V2	Q9X1V2 thermotoga
104	21	100.0	117	1	NU3M_BRALA	NU3M_BRALA

ID	TKN4_PSECU	STANDARD;	PRT;	11 AA.
105	21	100.0	117	2
106	21	100.0	117	2
107	21	100.0	117	2
108	21	100.0	118	2
109	21	100.0	119	2
110	21	100.0	121	2
111	21	100.0	123	2
112	21	100.0	124	2
113	21	100.0	125	2
114	21	100.0	125	2
115	21	100.0	125	2
116	21	100.0	125	2
117	21	100.0	128	2
118	21	100.0	128	2
119	21	100.0	128	2
120	21	100.0	128	2
121	21	100.0	129	1
122	21	100.0	129	1
123	21	100.0	129	2
124	21	100.0	130	1
125	21	100.0	130	1
126	21	100.0	130	1
127	21	100.0	130	1
128	21	100.0	130	1
129	21	100.0	131	1
130	21	100.0	131	2
131	21	100.0	131	2
132	21	100.0	132	1
133	21	100.0	132	1
134	21	100.0	132	2
135	21	100.0	132	2
136	21	100.0	133	2
137	21	100.0	133	2
138	21	100.0	134	1
139	21	100.0	134	1
140	21	100.0	134	1
141	21	100.0	134	2
142	21	100.0	134	2
143	21	100.0	134	2
144	21	100.0	134	2
145	21	100.0	136	1
146	21	100.0	136	2
147	21	100.0	137	1
148	21	100.0	137	2
149	21	100.0	137	2
150	21	100.0	137	2

## ALIGNMENTS

RESULT 1  
TKN4\_PSECU STANDARD; PRT; 11 AA.

AC P42959;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 05-JUL-2004 (Rel. 44, Last sequence update)  
DE Substance P-like peptide I (PG-SP1).  
OS Pseudophryne guentheri (Guenther's toadlet).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Myobatrachidae;  
OC Myobatrachinae; Pseudophryne.  
OX NCBI\_TaxID=30349;  
RN [1]  
RP SEQUENCE.  
RX TISSUE=Skin secretion;  
RA Simmaco M., Severini C., de Biase D., Barra D., Bosca F.,  
RT "Six novel tachykinin- and bombesin-related peptides from the skin of  
the Australian frog Pseudophryne guentheri.",  
Peptides 11:299-304(1990).

CC -1- FUNCTION: Tachykinins are active peptides which excite neurons,  
CC evoke behavioral responses, are potent vasodilators and  
CC secretagogues, and contract (directly or indirectly) many smooth  
CC muscles.  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- TISSUE SPECIFICITY: Skin.  
CC -1- SIMILARITY: Belongs to the tachykinin family.  
DR PIR: E60409; E60409.  
DR InterPro: IPR002040; Tachy Neurokinin.  
DR Pfam: PR02202; Tachykinin; 1.  
DR SMART: SM00203; TK; 1.  
DR PROSITE: PS00267; TACHYKININ, 1.  
KW Amidation; Amphibian defense peptide; Direct protein sequencing;  
KW Neuropeptide; Pyrrolidone carboxylic acid; Tachykinin.  
FT MOD RES 1 1  
FT MOD RES 11 11  
SQ SEQUENCE 11 AA; 1294 MW; 3A247C2CC9CB1A87 CRC64;

Query Match 100.0%; Score 21; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FGLM 4  
DB 8 FGLM 11

## RESULT 2

TKN5\_PSECU STANDARD; PRT; 11 AA.

AC P42959;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 05-JUL-2004 (Rel. 44, Last sequence update)  
DE Substance P-like peptide II (PG-SP11).  
OS Pseudophryne guentheri (Guenther's toadlet).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Myobatrachidae;  
OC Myobatrachinae; Pseudophryne.  
OX NCBI\_TaxID=30349;  
RN [1]  
RP SEQUENCE.  
RX TISSUE=Skin secretion;  
RA Simmaco M., Severini C., de Biase D., Barra D., Bosca F.,  
RT "Six novel tachykinin- and bombesin-related peptides from the skin of  
the Australian frog Pseudophryne guentheri.",  
Peptides 11:299-304(1990).

CC -1- FUNCTION: Tachykinins are active peptides which excite neurons,  
CC evoke behavioral responses, are potent vasodilators and  
CC secretagogues, and contract (directly or indirectly) many smooth  
CC muscles.  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- TISSUE SPECIFICITY: Skin.  
CC -1- SIMILARITY: Belongs to the tachykinin family.  
DR PIR: F60409; F60409.  
DR InterPro: IPR002040; Tachy Neurokinin.  
DR Pfam: PR02202; Tachykinin; 1.  
DR PROSITE: PS00267; TACHYKININ, 1.  
KW Amidation; Amphibian defense peptide; Direct protein sequencing;  
KW Neuropeptide; Pyrrolidone carboxylic acid; Tachykinin.  
FT MOD RES 1 1  
FT MOD RES 11 11  
SQ SEQUENCE 11 AA; 1293 MW; 3A247C2CC9CB1A57 CRC64;

Query Match 100.0%; Score 21; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FGLM 4  
DB 8 FGLM 11

GenCore version 5.1.6  
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## OM protein - protein search, using SW model

Run on: October 26, 2005, 08:04:16 ; Search time 10.6667 Seconds  
(without alignments)  
36.081 Million cell updates/sec

Title: US-10-053-669-2  
Perfect score: 21  
Sequence: 1 FGLM 4

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 150 summaries

Database : PIR 79:.\*  
1: p1r1:.\*  
2: p1r2:.\*  
3: p1r3:.\*  
4: p1r4:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21	100.0	11	1 A60654	substance P - guin
2	21	100.0	11	1 SPHO	substance P - hors
3	21	100.0	11	2 JN0023	substance P - chic
4	21	100.0	11	2 S33300	probable substance
5	21	100.0	11	2 E60409	substance P-like P
6	21	100.0	11	2 E60409	substance P-like P
7	21	100.0	11	2 S23308	substance P - rain
8	21	100.0	19	2 P80332	phospholipase A2 (
9	21	100.0	56	2 A69983	hypothetical prote
10	21	100.0	63	2 JC2412	tachykinin gamma c
11	21	100.0	69	2 S04666	hypothetical prote
12	21	100.0	72	2 JC5455	preprotachykinin-A
13	21	100.0	72	2 T52742	tachykinin A gamma
14	21	100.0	72	2 T25860	hypothetical prote
15	21	100.0	78	2 AE3165	hypothetical prote
16	21	100.0	80	2 T11069	NADH2 dehydrogenas
17	21	100.0	85	2 H69191	hypothetical prote
18	21	100.0	89	2 S72598	sulfate permease T
19	21	100.0	90	2 C85905	hypothetical prote
20	21	100.0	90	2 E91060	hypothetical prote
21	21	100.0	90	2 A65037	hypothetical prote
22	21	100.0	97	2 S12958	tachykinin delta p
23	21	100.0	102	2 G72756	hypothetical prote
24	21	100.0	105	2 F72614	hypothetical prote
25	21	100.0	106	2 G81275	hypothetical prote
26	21	100.0	109	2 I52333	G1 phase-specific
27	21	100.0	110	2 G69609	cytochrome-c oxida
28	21	100.0	112	1 SPRTA	substance P alpha
29	21	100.0	112	2 T51238	scarcrow-like pro

30	21	100.0	115	1 SPRBG	substance P gamma
31	21	100.0	115	2 S47039	tachykinin 1 precu
32	21	100.0	116	2 H83167	hypothetical prote
33	21	100.0	116	2 C72232	hypothetical prote
34	21	100.0	117	2 A71391	NADH2 dehydrogenas
35	21	100.0	117	2 G64486	hypothetical prote
36	21	100.0	117	2 B86771	hypothetical prote
37	21	100.0	114	2 E97098	Zn-finger containt
38	21	100.0	126	2 S70624	cytochrome P450 CY
39	21	100.0	128	2 A88072	protein ZK1240.6 [
40	21	100.0	129	1 SPHRB	neurokinin 1 precu
41	21	100.0	129	2 A82227	conserved hypothet
42	21	100.0	130	1 SPBOB	neurokinin 1 precu
43	21	100.0	130	1 SPRTB	substance P beta P
44	21	100.0	130	2 S47038	tachykinin 1 precu
45	21	100.0	130	2 T52526	neurokinin 1 precu
46	21	100.0	131	2 AG0070	conserved hypothet
47	21	100.0	132	2 AD0895	probable membrane
48	21	100.0	133	2 C24925	lactose permease -
49	21	100.0	133	2 G69137	DNA-dependent RNA
50	21	100.0	134	2 H65098	hypothetical prote
51	21	100.0	134	2 D85971	hypothetical prote
52	21	100.0	134	2 E91126	hypothetical prote
53	21	100.0	134	2 T43561	probable transposa
54	21	100.0	136	2 S04226	hemoglobin II - C1
55	21	100.0	137	1 R5YM16	ribosomal protein
56	21	100.0	138	2 G82915	ribosomal protein
57	21	100.0	145	2 H70946	hypothetical prote
58	21	100.0	147	2 AC1223	ethanolamine utill
59	21	100.0	147	2 AF1576	ethanolamine utill
60	21	100.0	152	2 T03456	cobd protein - Rho
61	21	100.0	154	2 B72317	hypothetical prote
62	21	100.0	155	2 B83004	hypothetical prote
63	21	100.0	160	2 G83300	hypothetical prote
64	21	100.0	163	2 T36985	hypothetical prote
65	21	100.0	166	2 AG1931	hypothetical prote
66	21	100.0	167	2 T11465	NADH2 dehydrogenas
67	21	100.0	168	2 T03141	hypothetical prote
68	21	100.0	169	2 P00185	conoplact intrinsi
69	21	100.0	169	2 E87657	hypothetical prote
70	21	100.0	172	2 T20329	hypothetical prote
71	21	100.0	173	2 E83931	hypothetical prote
72	21	100.0	174	2 E82122	purine-binding che
73	21	100.0	176	2 T45308	hypothetical prote
74	21	100.0	177	2 T01346	hypothetical prote
75	21	100.0	177	2 T45675	hypothetical prote
76	21	100.0	180	2 S77046	hypothetical prote
77	21	100.0	185	1 A59351	lysosyme (EC 3.2.1
78	21	100.0	185	1 LZGSG	lysosyme (EC 3.2.1
79	21	100.0	185	1 LZOGG	lysosyme (EC 3.2.1
80	21	100.0	185	1 LZMSG	lysosyme (EC 3.2.1
81	21	100.0	185	2 UC7955	lysosyme (EC 3.2.1
82	21	100.0	185	2 A59488	lysosyme g - Chine
83	21	100.0	185	2 A96615	probable dirigent
84	21	100.0	189	2 F82969	hypothetical prote
85	21	100.0	194	2 G71698	lipoprotein signal
86	21	100.0	196	2 S45553	spore maturation p
87	21	100.0	200	2 B71879	hypothetical prote
88	21	100.0	200	2 E64636	hypothetical prote
89	21	100.0	206	2 S56133	dicarboxylate tran
90	21	100.0	206	2 F97769	signal peptidase I
91	21	100.0	207	2 G96609	cytochrome-c oxida
92	21	100.0	209	1 C69796	conserved hypothet
93	21	100.0	210	2 F64115	hypothetical prote
94	21	100.0	210	2 T40465	probable mitosis a
95	21	100.0	211	2 S18463	lysosyme (EC 3.2.1
96	21	100.0	213	2 G72276	phosphoribosylform
97	21	100.0	214	2 AG2684	RtB family transp
98	21	100.0	215	2 AD0681	probable ABC trans
99	21	100.0	215	2 T22446	hypothetical prote
100	21	100.0	216	2 AH0120	probable membrane
101	21	100.0	217	2 F83840	stage II sporulati
102	21	100.0	220	2 A95362	probable inner-mem

103 21 100.0 221 2 A10360 conserved hypochet  
 104 21 100.0 223 2 C81397 phosphoribosylform  
 105 21 100.0 223 2 H81219 NADH dehydrogenase  
 106 21 100.0 223 2 B81391 NADH dehydrogenase  
 107 21 100.0 224 2 C69687 menaquinol-cytochr  
 108 21 100.0 224 2 B29503 hypochetrical prote  
 109 21 100.0 224 2 E97466 hypochetrical prote  
 110 21 100.0 228 2 E86849 glutamate ABC tran  
 111 21 100.0 228 2 AD1024 conserved hypochet  
 112 21 100.0 229 2 H97147 enoyl-CoA hydratase  
 113 21 100.0 230 1 H64634 conserved hypochet  
 114 21 100.0 230 2 F71879 hypochetrical prote  
 115 21 100.0 231 2 A75462 conserved hypochet  
 116 21 100.0 231 2 H75465 hypochetrical prote  
 117 21 100.0 232 1 B70167 conserved hypochet  
 118 21 100.0 232 2 JC5010 nucleotide-binding  
 119 21 100.0 232 2 H69294 conserved hypochet  
 120 21 100.0 233 2 C71848 purine nucleoside  
 121 21 100.0 233 2 AH1218 Salmonella typhimu  
 122 21 100.0 234 2 F75254 conserved hypochet  
 123 21 100.0 235 2 G69882 hypochetrical prote  
 124 21 100.0 235 2 F71249 hypochetrical prote  
 125 21 100.0 236 2 A75455 hypochetrical prote  
 126 21 100.0 237 1 S76661 hypochetrical prote  
 127 21 100.0 239 2 S40143 nitrate transporte  
 128 21 100.0 239 2 AE0772 probable exported  
 129 21 100.0 240 2 H70091 hypochetrical prote  
 130 21 100.0 242 1 F64123 dehydrobiotin synth  
 131 21 100.0 242 2 JC5883 myocyte enhancer f  
 132 21 100.0 243 2 AG2395 hypochetrical prote  
 133 21 100.0 245 2 E81023 ABC transporter, A  
 134 21 100.0 245 2 E81968 probable ABC trans  
 135 21 100.0 246 2 H84127 enoyl CoA hydratase  
 136 21 100.0 247 2 H69493 phosphoenolpyruvate-  
 137 21 100.0 247 2 E82555 heme ABC transport  
 138 21 100.0 248 2 F75200 hypochetrical prote  
 139 21 100.0 249 2 A71234 hypochetrical prote  
 140 21 100.0 251 2 B84016 hypochetrical prote  
 141 21 100.0 253 2 C82517 conserved hypochet  
 142 21 100.0 255 2 G75157 abc transporter, A  
 143 21 100.0 256 2 J01106 tonoplast intrinsi  
 144 21 100.0 256 2 S26742 tonoplast intrinsi  
 145 21 100.0 256 2 D81181 conserved hypochet  
 146 21 100.0 256 2 C81925 probable sec-indep  
 147 21 100.0 259 2 B83838 oxidoreductase Bhl  
 148 21 100.0 259 2 D83216 probable aldolase  
 149 21 100.0 261 2 C86207 hypochetrical prote  
 150 21 100.0 265 2 G70888 hypochetrical prote

## ALIGNMENTS

## RESULT 1

A60654

substance P - guinea pig

C/Species: Cavia porcellus (guinea pig)  
 C/Date: 14-May-1993 #sequence\_revision 27-Jun-1994 #text\_change 09-Jul-2004  
 C/Accession: A60654

R/Murphy, R.

Neuropeptides 14, 105-110, 1989

A/Title: Primary amino acid sequence of guinea-pig substance P.

A/Reference number: A60654; MUID:90044685; PMID:2478925

A/Accession: A60654

A/Molecule type: protein

A/Residues: 1-11 &lt;MUR&gt;

A/Cross-references: UNIPROT:P01290

C/Superfamily: substance P precursor

C/Keywords: amidated carboxyl end; neuropeptide; tachykinin

F/11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 100.0%; Score 21; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 19;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 FGLM 4  
 ||||  
 Db 8 FGLM 11

## RESULT 2

SPHO

substance P - horse

C/Species: Equus caballus (domestic horse)

C/Date: 23-Oct-1981 #sequence\_revision 23-Oct-1981 #text\_change 09-Jul-2004

C/Accession: A01558

R/Studer, R.O.; Tirzeliak, A.; Lergier, W.

Helv. Chim. Acta 56, 860-866, 1973

A/Title: Isolierung und Aminosäuresequenz von Substanz P aus Pferdedarm.

A/Reference number: A01558

A/Accession: A01558

A/Molecule type: protein

A/Residues: 1-11 &lt;STU&gt;

A/Cross-references: UNIPROT:P01290

C/Superfamily: substance P precursor

C/Keywords: amidated carboxyl end; hormone

Query Match 100.0%; Score 21; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 19;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FGLM 4  
 ||||  
 Db 8 FGLM 11

## RESULT 3

JN0023

substance P - chicken

C/Species: Gallus gallus (chicken)

C/Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 09-Jul-2004  
 C/Accession: JN0023

R/Conlon, J.M.; Katsoulis, S.; Schmidt, W.E.; Thim, L.

Regul. Pept. 20, 171-180, 1988

A/Title: [Arg3]substance P and neurokinin A from chicken small intestine.

A/Reference number: JN0023; MUID:88204263; PMID:2452461

A/Accession: JN0023

A/Molecule type: protein

A/Residues: 1-11 &lt;CON&gt;

A/Cross-references: UNIPROT:P19850

C/Superfamily: substance P precursor

C/Keywords: amidated carboxyl end; tachykinin

Query Match 100.0%; Score 21; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 19;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FGLM 4  
 ||||  
 Db 8 FGLM 11

## RESULT 4

S33300

probable substance P - smaller spotted catshark

C/Species: Scyliorhinus canicula (smaller spotted catshark, smaller spotted dogfish)

C/Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 09-Jul-2004

C/Accession: S33300

R/Waugh, D.; Wang, Y.; Hazon, N.; Balmont, R.J.; Conlon, J.M.

Eur. J. Biochem. 214, 469-474, 1993

A/Title: Primary structures and biological activities of substance-P-related peptides from

A/Reference number: S33300; MUID:93392508; PMID:7685693

A/Accession: S33300  
 A/Molecule type: protein



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 26, 2005, 08:05:47 ; Search time 99.5556 Seconds  
(without alignments)  
16.775 Million cell updates/sec

Title: ~~US-10-053-669-2~~  
Perfect score: 21  
Sequence: 1 FGLM 4

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1862994 seqs, 417510619 residues

Total number of hits satisfying chosen parameters: 1862994

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 150 summaries

Database ~~US-10-053-669-2~~  
Published/Unpublished/Other: ~~XXXXXX~~  
1: /cgn2\_6/prodata/1/pubppa/US07\_PUBCOMB.pep:\*  
2: /cgn2\_6/prodata/1/pubppa/PCR\_NEW\_PUB.pep:\*  
3: /cgn2\_6/prodata/1/pubppa/US06\_NEW\_PUB.pep:\*  
4: /cgn2\_6/prodata/1/pubppa/US06\_PUBCOMB.pep:\*  
5: /cgn2\_6/prodata/1/pubppa/US07\_NEW\_PUB.pep:\*  
6: /cgn2\_6/prodata/1/pubppa/PCRUS\_PUBCOMB.pep:\*  
7: /cgn2\_6/prodata/1/pubppa/US08\_NEW\_PUB.pep:\*  
8: /cgn2\_6/prodata/1/pubppa/US08\_PUBCOMB.pep:\*  
9: /cgn2\_6/prodata/1/pubppa/US09\_PUBCOMB.pep:\*  
10: /cgn2\_6/prodata/1/pubppa/US09\_PUBCOMB.pep:\*  
11: /cgn2\_6/prodata/1/pubppa/US09C\_PUBCOMB.pep:\*  
12: /cgn2\_6/prodata/1/pubppa/US09C\_NEW\_PUB.pep:\*  
13: /cgn2\_6/prodata/1/pubppa/US10\_PUBCOMB.pep:\*  
14: /cgn2\_6/prodata/1/pubppa/US10\_PUBCOMB.pep:\*  
15: /cgn2\_6/prodata/1/pubppa/US10C\_PUBCOMB.pep:\*  
16: /cgn2\_6/prodata/1/pubppa/US10C\_PUBCOMB.pep:\*  
17: /cgn2\_6/prodata/1/pubppa/US10E\_PUBCOMB.pep:\*  
18: /cgn2\_6/prodata/1/pubppa/US10E\_NEW\_PUB.pep:\*  
19: /cgn2\_6/prodata/1/pubppa/US11\_PUBCOMB.pep:\*  
20: /cgn2\_6/prodata/1/pubppa/US11\_NEW\_PUB.pep:\*  
21: /cgn2\_6/prodata/1/pubppa/US60\_NEW\_PUB.pep:\*  
22: /cgn2\_6/prodata/1/pubppa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	21	100.0	4	9 US-09-265-690C-2	Sequence 2, Appl1
2	21	100.0	4	14 US-10-230-133-3	Sequence 3, Appl1
3	21	100.0	4	14 US-10-053-669-2	Sequence 2, Appl1
4	21	100.0	4	16 US-10-695-536-3	Sequence 3, Appl1
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; APPLICANT: Wellb, Ibert
; TITLE OF INVENTION: Method for Detecting Deficient Cellular Membrane Tightly Bound Mac
; FILE REFERENCE: 1427001
; CURRENT APPLICATION NUMBER: US/09/265,690C
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
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; TYPE: PRT
; ORGANISM: Homo sapiens
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; LOCATION: (4)..(4)
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Best Local Similarity 100.0%; Pred.No. 1.7e+06;
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; TITLE OF INVENTION: Antagonists of the magnesium binding defect as therapy agents and
; FILE REFERENCE: 2892-106
; CURRENT APPLICATION NUMBER: US/10/230,133
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 09/635,266
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
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; TYPE: PRT
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; Publication No. US20030077658A1
; GENERAL INFORMATION:
; APPLICANT: Wellb, Ibert
; TITLE OF INVENTION: Method for Detecting Deficient Cellular Membrane Tightly Bound Mac
; FILE REFERENCE: N1427-005
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 26, 2005, 08:04:31 ; Search time 26.6667 Seconds  
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Listing first 150 summaries

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98	21	100.0	12	3	US-09-264-709A-16 Sequence 16, Appl
99	21	100.0	12	3	US-08-505-250-27 Sequence 27, Appl
100	21	100.0	12	3	US-08-505-250-53 Sequence 53, Appl

101 21 100.0 12 4 US-09-922-093-2 Sequence 2, Appl1  
 102 21 100.0 12 4 US-09-922-093-5 Sequence 5, Appl1  
 103 21 100.0 12 4 US-09-922-093-8 Sequence 8, Appl1  
 104 21 100.0 12 4 US-09-403-752A-41 Sequence 41, Appl1  
 105 21 100.0 12 4 US-09-763-669-1 Sequence 1, Appl1  
 106 21 100.0 12 4 US-09-763-669-2 Sequence 2, Appl1  
 107 21 100.0 12 4 US-09-625-098F-2 Sequence 2, Appl1  
 108 21 100.0 12 4 US-09-625-098F-5 Sequence 5, Appl1  
 109 21 100.0 12 4 US-09-428-692-22 Sequence 8, Appl1  
 110 21 100.0 12 4 US-09-428-692-25 Sequence 22, Appl1  
 111 21 100.0 12 4 US-09-428-692-28 Sequence 25, Appl1  
 112 21 100.0 12 4 US-09-551-151A-41 Sequence 28, Appl1  
 113 21 100.0 12 4 US-09-551-151A-41 Sequence 41, Appl1  
 114 21 100.0 12 5 PCT-US92-06532-4 Sequence 4, Appl1  
 115 21 100.0 12 5 PCT-US95-05600-24 Sequence 24, Appl1  
 116 21 100.0 13 1 US-07-712-828B-5 Sequence 5, Appl1  
 117 21 100.0 13 4 US-09-922-093-3 Sequence 5, Appl1  
 118 21 100.0 13 4 US-09-922-093-6 Sequence 6, Appl1  
 119 21 100.0 13 4 US-09-922-093-9 Sequence 6, Appl1  
 120 21 100.0 13 4 US-09-625-098F-3 Sequence 9, Appl1  
 121 21 100.0 13 4 US-09-625-098F-6 Sequence 3, Appl1  
 122 21 100.0 13 4 US-09-625-098F-9 Sequence 6, Appl1  
 123 21 100.0 13 4 US-09-428-692-23 Sequence 9, Appl1  
 124 21 100.0 13 4 US-09-428-692-26 Sequence 23, Appl1  
 125 21 100.0 13 4 US-09-428-692-29 Sequence 26, Appl1  
 126 21 100.0 14 4 US-09-922-093-4 Sequence 29, Appl1  
 127 21 100.0 14 4 US-09-922-093-7 Sequence 4, Appl1  
 128 21 100.0 14 4 US-09-922-093-10 Sequence 7, Appl1  
 129 21 100.0 14 4 US-09-625-098F-4 Sequence 10, Appl1  
 130 21 100.0 14 4 US-09-625-098F-7 Sequence 4, Appl1  
 131 21 100.0 14 4 US-09-625-098F-10 Sequence 7, Appl1  
 132 21 100.0 14 4 US-09-428-692-24 Sequence 10, Appl1  
 133 21 100.0 14 4 US-09-428-692-27 Sequence 27, Appl1  
 134 21 100.0 14 4 US-09-428-692-30 Sequence 30, Appl1  
 135 21 100.0 20 3 US-08-468-514-1 Sequence 1, Appl1  
 136 21 100.0 20 3 US-08-890-157A-2 Sequence 2, Appl1  
 137 21 100.0 20 3 US-08-505-250-50 Sequence 50, Appl1  
 138 21 100.0 20 3 US-08-505-250-50 Sequence 50, Appl1  
 139 21 100.0 20 4 US-09-570-022-23 Sequence 23, Appl1  
 140 21 100.0 21 1 US-08-468-514-4 Sequence 4, Appl1  
 141 21 100.0 22 1 US-08-468-514-11 Sequence 11, Appl1  
 142 21 100.0 61 4 US-09-270-767-363A8 Sequence 363A8, A  
 143 21 100.0 61 4 US-09-270-767-51565 Sequence 51565, A  
 144 21 100.0 65 4 US-09-148-545-171 Sequence 171, App  
 145 21 100.0 68 4 US-09-902-540-11170 Sequence 11170, A  
 146 21 100.0 70 4 US-09-248-796A-25823 Sequence 25823, A  
 147 21 100.0 72 4 US-09-489-039A-11664 Sequence 11664, A  
 148 21 100.0 73 4 US-09-489-039A-11664 Sequence 9299, Ap  
 149 21 100.0 78 3 US-09-134-001C-3647 Sequence 3647, Ap  
 150 21 100.0 78 4 US-09-540-236-2303 Sequence 2303, Ap

## ALIGNMENTS

RESULT 1  
 US-08-441-591-63  
 ; Sequence 63, Application US/08441591  
 ; Patent No. 5637682  
 ; GENERAL INFORMATION:  
 ; APPLICANT: NIEWLANDT, D., GOLD, L. AND WECKER, M.  
 ; TITLE OF INVENTION: HIGH-AFFINITY  
 ; TITLE OF INVENTION: OLIGONUCLEOTIDE LIGANDS  
 ; TITLE OF INVENTION: TO THE TACHYKININ  
 ; TITLE OF INVENTION: SUBSTANCE P  
 ; NUMBER OF SEQUENCES: 66  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Swanson & Bratschun, L.L.C.  
 ; STREET: 8400 E. Prentice Avenue, Suite 200  
 ; CITY: Englewood  
 ; STATE: Colorado  
 ; COUNTRY: USA  
 ; ZIP: 80111

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MG storage  
 COMPUTER: IBM compatible  
 OPERATING SYSTEM: MS-DOS  
 SOFTWARE: Wordperfect 5.1  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/441,591  
 FILING DATE:  
 CLASSIFICATION: 435  
 PRIOR APPLICATION NUMBER: 08/303,362  
 FILING DATE: 9-SEPTEMBER-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 07/714,131  
 FILING DATE: 10-JUNE-1991  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 07/931,473  
 FILING DATE: 17-AUGUST-1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/117,991  
 FILING DATE: 8-SEPTEMBER 1993  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 07/536,428  
 FILING DATE: 11-JUNE-1990  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 07/964,624  
 FILING DATE: 21-OCTOBER-1992  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Barry J. Swanson  
 REGISTRATION NUMBER: 33,215  
 REFERENCE/DOCKET NUMBER: NEX21/C  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (303) 793-3333  
 TELEFAX: (303) 793-3433  
 INFORMATION FOR SEQ ID NO: 63:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 4  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 US-08-441-591-63

Query Match 100.0%; Score 21; DB 1; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 4.1e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FGLM 4  
 Db 1 FGLM 4

RESULT 2  
 US-08-303-362A-63  
 ; Sequence 63, Application US/08303362A  
 ; Patent No. 5648214  
 ; GENERAL INFORMATION:  
 ; APPLICANT: NIEWLANDT, D., GOLD, L. AND WECKER, M.  
 ; TITLE OF INVENTION: HIGH-AFFINITY  
 ; TITLE OF INVENTION: OLIGONUCLEOTIDE LIGANDS  
 ; TITLE OF INVENTION: TO THE TACHYKININ  
 ; TITLE OF INVENTION: SUBSTANCE P  
 ; NUMBER OF SEQUENCES: 66  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Swanson & Bratschun, L.L.C.  
 ; STREET: 8400 E. Prentice Avenue, Suite 200  
 ; CITY: Englewood  
 ; STATE: Colorado  
 ; COUNTRY: USA  
 ; ZIP: 80111  
 ; COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MG storage  
 COMPUTER: IBM compatible  
 OPERATING SYSTEM: MS-DOS

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 26, 2005, 08:00:50 ; Search time 57.7778 Seconds  
(without alignments)  
26.776 Million cell updates/sec

Title: **US-10-053-669-2**

Perfect score: 21  
Sequence: 1 FGLM 4

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues  
Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match -0%  
Maximum Match 100%  
Listing first 150 summaries

Date/Database: 1: Geneseqp1980s:.\*  
2: Geneseqp1990s:.\*  
3: Geneseqp2000s:.\*  
4: Geneseqp2001s:.\*  
5: Geneseqp2002s:.\*  
6: Geneseqp2003as:.\*  
7: Geneseqp2003bs:.\*  
8: Geneseqp2004s:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21	100.0	4	2 AAW41683	AAW41683 Peptide u
2	21	100.0	4	2 AAY31075	AAY31075 Non-cross
3	21	100.0	4	3 AAB23026	AAB23026 Human/rat
4	21	100.0	4	3 AAY67577	AAY67577 P antigen
5	21	100.0	4	4 AAB91447	AAB91447 Tachykinin
6	21	100.0	4	4 AAB10091	AAB10091 Substance
7	21	100.0	4	5 AAB77846	AAB77846 Tachykinin
8	21	100.0	4	5 ADE94198	ADe94198 High acti
9	21	100.0	4	8 ADR43772	ADr43772 Human mag
10	21	100.0	5	2 AAR33009	AAR33009 Alpha-sub
11	21	100.0	5	2 AAR33008	AAR33008 Alpha-sub
12	21	100.0	5	2 AAR33007	AAR33007 Alpha-sub
13	21	100.0	5	2 AAR33010	AAR33010 Alpha-sub
14	21	100.0	5	2 AAR54549	AAR54549 Cholecynt
15	21	100.0	5	2 AAR54551	AAR54551 Cholecynt
16	21	100.0	5	2 AAR54550	AAR54550 Cholecynt
17	21	100.0	5	2 AAR54548	AAR54548 Cholecynt
18	21	100.0	5	2 AAW41687	AAW41687 Tetrapept
19	21	100.0	5	2 AAW99643	AAW99643 Substance
20	21	100.0	5	2 AAY50325	AAY50325 Neutrophil
21	21	100.0	5	2 AAW92660	AAW92660 Human tac
22	21	100.0	5	2 AAW92702	AAW92702 Human tac
23	21	100.0	5	3 AAB23025	AAB23025 Human/rat
24	21	100.0	5	3 AAY67576	AAY67576 P antigen
25	21	100.0	5	4 AAB91428	AAB91428 Tachykinin

26	21	100.0	5	4 AAB91389	AAB91389 Tachykinin
27	21	100.0	5	5 AAB10090	ABb10090 Substance
28	21	100.0	5	5 ABB10089	ABb10089 Substance
29	21	100.0	5	5 ABB10088	ABb10088 Substance
30	21	100.0	5	5 AAB77845	AAB77845 Tachykinin
31	21	100.0	5	7 ADE94205	ADe94205 High acti
32	21	100.0	5	7 ADE94203	ADe94203 High acti
33	21	100.0	5	7 ADE94204	ADe94204 High acti
34	21	100.0	5	7 ADF92530	ADf92530 Substance
35	21	100.0	5	8 ADR95078	ADr95078 Mammalian
36	21	100.0	5	8 ADR93603	ADr93603 E. coli m
37	21	100.0	5	8 ADR43771	ADr43771 Human mag
38	21	100.0	6	1 AAP40519	AAp40519 Sequence
39	21	100.0	6	1 AAP50694	AAp50694 Sequence
40	21	100.0	6	1 AAP50632	AAp50632 Substance
41	21	100.0	6	1 AAP61486	AAp61486 Peptide h
42	21	100.0	6	2 AAR07893	AAR07893 Cyclopept
43	21	100.0	6	2 AAR07889	AAR07889 Cyclopept
44	21	100.0	6	2 AAR21959	AAR21959 Substance
45	21	100.0	6	2 AAR27690	AAR27690 Cyclic ta
46	21	100.0	6	2 AAR27694	AAR27694 Cyclic ta
47	21	100.0	6	2 AAR27691	AAR27691 Cyclic ta
48	21	100.0	6	2 AAW99692	AAW99692 Substance
49	21	100.0	6	2 AAW99686	AAW99686 Substance
50	21	100.0	6	2 AAW92706	AAW92706 Human tac
51	21	100.0	6	2 AAW92659	AAW92659 Human tac
52	21	100.0	6	3 AAB03356	ABb03356 Neurokinin
53	21	100.0	6	3 AAY67575	AAY67575 P antigen
54	21	100.0	6	3 AAY7917	AAy7917 Neurokinin
55	21	100.0	6	3 AAY7947	AAy7947 Neurokinin
56	21	100.0	6	3 AAY97932	AAy97932 Neurokinin
57	21	100.0	6	4 AAB82453	ABb82453 Fluorinat
58	21	100.0	6	4 AAB82436	ABb82436 Fluorinat
59	21	100.0	6	4 AAB91421	ABb91421 Tachykinin
60	21	100.0	6	4 AAB81425	ABb81425 Tachykinin
61	21	100.0	6	4 AAB91390	ABb91390 Tachykinin
62	21	100.0	6	4 AAB91419	ABb91419 Tachykinin
63	21	100.0	6	4 AAG99351	AAg99351 Atypical
64	21	100.0	6	4 AAU07303	AAU07303 Neurokinin
65	21	100.0	6	4 AAB68998	ABb68998 Neurokinin
66	21	100.0	6	4 AAB88884	ABb88884 Chimeric
67	21	100.0	6	4 AAB88886	ABb88886 Chimeric
68	21	100.0	6	4 AAG67862	AAg67862 Neurokinin
69	21	100.0	6	5 AAB10086	ABb10086 Substance
70	21	100.0	6	7 ADB88521	ADb88521 Human NK-
71	21	100.0	6	7 ADE94202	ADe94202 High acti
72	21	100.0	6	7 AAG39528	AAg39528 Neurokinin
73	21	100.0	7	2 AAR21956	AAR21956 Substance
74	21	100.0	7	2 AAY50324	AAy50324 Neutrophil
75	21	100.0	7	2 AAW92662	AAW92662 Human tac
76	21	100.0	7	2 AAW92705	AAW92705 Human tac
77	21	100.0	7	3 AAY67574	AAY67574 P antigen
78	21	100.0	7	3 AAB80323	ABb80323 Human pro
79	21	100.0	7	4 AAB80324	ABb80324 Human pro
80	21	100.0	7	4 AAB91431	ABb91431 Tachykinin
81	21	100.0	7	4 AAB91420	ABb91420 Tachykinin
82	21	100.0	7	4 AAG99350	AAg99350 Atypical
83	21	100.0	7	4 AAB88845	ABb88845 Chimeric
84	21	100.0	7	5 AAB80950	ABb80950 Substance
85	21	100.0	7	5 ADE94201	ADe94201 High acti
86	21	100.0	7	7 ADF92529	ADf92529 Substance
87	21	100.0	7	8 ADR95077	ADr95077 Mammalian
88	21	100.0	8	1 AAP20303	AAp20303 Gastric
89	21	100.0	8	2 AAR28444	AAR28444 Neurokinin
90	21	100.0	8	2 AAW92664	AAW92664 Human tac
91	21	100.0	8	2 AAW92710	AAW92710 Human tac
92	21	100.0	8	3 AAY67573	AAY67573 P antigen
93	21	100.0	8	4 AAB91407	ABb91407 Tachykinin
94	21	100.0	8	4 AAB91416	ABb91416 Tachykinin
95	21	100.0	8	4 AAB91424	ABb91424 Tachykinin
96	21	100.0	8	4 AAG99349	AAg99349 Atypical
97	21	100.0	8	5 AAB909498	ABb909498 Substance

99	21	100.0	8	7	ADB94200	AdB94200 High acti
100	21	100.0	9	1	AAP50634	Aap50634 Substance
101	21	100.0	9	2	AAW92714	Aaw92714 Human tac
102	21	100.0	9	4	AAB80325	Aab80325 Human pro
103	21	100.0	9	4	AAB91446	Aab91446 Tachykinl
104	21	100.0	9	4	AAB91369	Aab91369 Tachykinl
105	21	100.0	9	4	AAG99348	Aag99348 Atypical
106	21	100.0	9	7	AAE38833	Aae38833 Membrane
107	21	100.0	9	7	ADF92528	Adf92528 Substance
108	21	100.0	9	8	ADOC4477	Adoc4477 Substance
109	21	100.0	9	8	ADN95076	Adn95076 Mammalian
110	21	100.0	9	8	ADS15335	Ads15335 Substance
111	21	100.0	10	1	AAP50633	Aap50633 Substance
112	21	100.0	10	2	AAE21933	Aae21933 Substance
113	21	100.0	10	2	AAE5181	Aae5181 S. cerevi
114	21	100.0	10	2	AAW99684	Aaw99684 Substance
115	21	100.0	10	2	AAV06939	Aav06939 Substance
116	21	100.0	10	2	AAW92663	Aaw92663 Human tac
117	21	100.0	10	4	AAB66675	Aab66675 Tachykinl
118	21	100.0	10	4	AAB91445	Aab91445 Tachykinl
119	21	100.0	10	4	AAAG9347	Aag9347 Atypical
120	21	100.0	10	4	AAAG64746	Aag64746 Substance
121	21	100.0	10	8	ADN12181	Adn12181 Antino aci
122	21	100.0	10	8	ADN27868	Adn27868 Trichomon
123	21	100.0	11	1	AAP61480	Aap61480 Sequence
124	21	100.0	11	1	AAP80312	Aap80312 Sequence
125	21	100.0	11	2	AAE1854	Aae1854 Undecapep
126	21	100.0	11	2	AAE13162	Aae13162 Sialic ac
127	21	100.0	11	2	AAE28442	Aae28442 Substance
128	21	100.0	11	2	AAE21969	Aae21969 Cyclic su
129	21	100.0	11	2	AAE21942	Aae21942 Substance
130	21	100.0	11	2	AAE21962	Aae21962 Substance
131	21	100.0	11	2	AAE21945	Aae21945 Substance
132	21	100.0	11	2	AAE21963	Aae21963 Substance
133	21	100.0	11	2	AAE21949	Aae21949 Substance
134	21	100.0	11	2	AAE21951	Aae21951 Substance
135	21	100.0	11	2	AAE21934	Aae21934 Substance
136	21	100.0	11	2	AAE21946	Aae21946 Substance
137	21	100.0	11	2	AAE21964	Aae21964 Substance
138	21	100.0	11	2	AAE21970	Aae21970 Cyclic su
139	21	100.0	11	2	AAE21938	Aae21938 Substance
140	21	100.0	11	2	AAE21941	Aae21941 Substance
141	21	100.0	11	2	AAE21943	Aae21943 Substance
142	21	100.0	11	2	AAE21954	Aae21954 Substance
143	21	100.0	11	2	AAE42646	Aae42646 Neurokinl
144	21	100.0	11	2	AAE85243	Aae85243 Substance
145	21	100.0	11	2	AAE77310	Aae77310 Substance
146	21	100.0	11	2	AAW33181	Aaw33181 Mono-DTPA
147	21	100.0	11	2	AAW33180	Aaw33180 Mono-DTPA
148	21	100.0	11	2	AAW04616	Aaw04616 Substance
149	21	100.0	11	2	AAW79775	Aaw79775 Substance
150	21	100.0	11	2	AAW42973	Aaw42973 Substrate

## ALIGNMENTS

RESULT 1  
ID AAW41683  
AAW41683 standard; peptide; 4 AA.

XX AAW41683;

DT 09-JUN-1998 (first entry)

DE Peptide used in ophthalmic drug to treat corneal disorders.

XX Ophthalmic drug; corneal disorder; ulcer; epithelial peeling; dry eye;

KW Keratitis; insulin like growth factor-I; IGF-I; eye drop.

OS Synthetic.

XX Key Location/Qualifiers

FT Modified-site 4 /note= "C-terminal amide"  
FT  
XX  
XX WO9749419-A1.  
PN  
XX  
XX 31-DEC-1997.  
PD  
XX  
XX  
PF 11-JUN-1997; 97WO-JP002015.  
XX  
XX  
PR 26-JUN-1996; 96JP-00165612.  
XX  
XX (SANTEN) SANTEN PHARM CO LTD.  
PA  
XX  
XX Nishida T, Nakamura M, Nakata K;  
XX  
XX WPI; 1998-076907/07.  
DR  
XX  
XX  
PT Ophthalmic drug composition containing tetrapeptide - is useful as  
PT corneal disorder remedy for corneal ulcer, corneal epithelial peeling,  
PT dry eye, keratitis.  
XX  
XX Claim 1; Page 15; 19pp; Japanese.  
PS  
XX  
XX The present sequence represents a tetrapeptide which is the active  
CC ingredient in an ophthalmic drug composition. It is used, together with  
CC insulin like growth factor-I (IGF-I), to treat corneal disorders such as  
CC corneal ulcer, corneal epithelial peeling, dry eye and keratitis. The  
CC dosage is 0.1-5000 (preferably 1-1000) mg/day of the tetrapeptide and  
CC 0.001-100 (preferably 0.01-10) mg/day of IGF-I. The preferable form of  
CC the composition is eye drops  
SQ  
XX Sequence 4 AA;

Query Match 100.0%; Score 21; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FGLM 4  
DB 1 FGLM 4

RESULT 2  
ID AAY31075  
AAY31075 standard; peptide; 4 AA.

AC AAY31075;

DT 21-OCT-1999 (first entry)

XX Non-crosslinked protein particle peptide 124.

KW Non-crosslinked protein particle; diagnostic; therapy; monodisperse;  
albumin; haemoglobin; nanometer; micrometer; clearance.

XX Synthetic.

XX Key Location/Qualifiers

FT Modified-site 4 /note= "C-terminal amide"

XX US5945033-A.

PD 31-AUG-1999.

PF 12-NOV-1996; 96US-00747137.

XX 15-JAN-1991; 91US-00641720.

PR 13-OCT-1992; 92US-00959560.

PR 01-JUN-1993; 93US-0069831.

PR 14-MAR-1994; 94US-00212546.

XX (HEMO-) HEMOSPHERE INC.

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 26, 2005, 08:12:17 ; Search time 99.556 Seconds  
(without alignments)  
20.575 Million cell updates/sec

Title: us-10-053-669-2  
Perfect score: 21  
Sequence: 1 FGLM 4

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 3223

Minimum (DB-seq-length): 0  
Maximum (DB-seq-length): 11

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 150 summaries

Database :

1: uniprot\_03:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21	100.0	11	1	TKN4_PSEGU
2	21	100.0	11	1	TKN5_PSEGU
3	21	100.0	11	1	TKNA_CALVO
4	21	100.0	11	1	TKNA_CHICK
5	21	100.0	11	1	TKNA_HORSE
6	21	100.0	11	1	TKNA_ONCMY
7	21	100.0	11	1	TKNA_SCYCA
8	18	85.7	10	1	TKN1_SCYCA
9	18	85.7	10	1	TKNB_RANCA
10	18	85.7	10	1	TKS1_AEDAE
11	18	85.7	10	1	TKS2_AEDAE
12	18	85.7	11	1	TKN1_UPEIN
13	18	85.7	11	1	TKN1_UPEIN
14	18	85.7	11	1	TKN2_UPEIN
15	18	85.7	11	1	TKNA_RANCA
16	18	85.7	11	1	TKNA_RANCA
17	18	85.7	11	1	TKN1_PHYFU
18	18	85.7	11	1	TKN1_PHYFU
19	18	85.7	11	1	TKN1_PHYFU
20	18	85.7	11	1	TKN1_PHYFU
21	18	85.7	11	1	TKN1_PHYFU
22	18	85.7	11	1	TKN1_PHYFU
23	18	85.7	11	1	TKN1_PHYFU
24	18	85.7	11	1	TKN1_PHYFU
25	18	85.7	11	1	TKN1_PHYFU
26	18	85.7	11	1	TKN1_PHYFU
27	18	85.7	11	1	TKN1_PHYFU
28	18	85.7	11	1	TKN1_PHYFU
29	18	85.7	11	1	TKN1_PHYFU
30	18	85.7	11	1	TKN1_PHYFU
31	18	85.7	11	1	TKN1_PHYFU

32	16	76.2	8	1	ALL4_CYPDO	P82155 cydia pomon
33	16	76.2	8	1	ALL5_CYPDO	P82156 cydia pomon
34	16	76.2	8	1	ALL6_CYPDO	P82157 cydia pomon
35	16	76.2	8	1	ALL7_CYPDO	P81809 carcius ma
36	16	76.2	8	1	ALL8_CYPDO	P81811 carcius ma
37	16	76.2	8	1	ALL9_CYPDO	P81813 carcius ma
38	16	76.2	9	1	ALL10_CYPDO	P81813 carcius ma
39	16	76.2	9	1	ALL11_CYPDO	P81813 carcius ma
40	16	76.2	9	2	ALL12_CYPDO	P81813 carcius ma
41	16	76.2	9	2	ALL13_CYPDO	P81813 carcius ma
42	16	76.2	10	2	ALL14_CYPDO	P81813 carcius ma
43	16	76.2	10	2	ALL15_CYPDO	P81813 carcius ma
44	16	76.2	10	2	ALL16_CYPDO	P81813 carcius ma
45	16	76.2	10	2	ALL17_CYPDO	P81813 carcius ma
46	16	76.2	10	2	ALL18_CYPDO	P81813 carcius ma
47	16	76.2	10	2	ALL19_CYPDO	P81813 carcius ma
48	16	76.2	10	2	ALL20_CYPDO	P81813 carcius ma
49	16	76.2	10	2	ALL21_CYPDO	P81813 carcius ma
50	16	76.2	10	2	ALL22_CYPDO	P81813 carcius ma
51	16	76.2	10	2	ALL23_CYPDO	P81813 carcius ma
52	16	76.2	10	2	ALL24_CYPDO	P81813 carcius ma
53	16	76.2	10	2	ALL25_CYPDO	P81813 carcius ma
54	16	76.2	10	2	ALL26_CYPDO	P81813 carcius ma
55	16	76.2	10	2	ALL27_CYPDO	P81813 carcius ma
56	16	76.2	10	2	ALL28_CYPDO	P81813 carcius ma
57	16	76.2	10	2	ALL29_CYPDO	P81813 carcius ma
58	16	76.2	10	2	ALL30_CYPDO	P81813 carcius ma
59	16	76.2	10	2	ALL31_CYPDO	P81813 carcius ma
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62	16	76.2	10	2	ALL34_CYPDO	P81813 carcius ma
63	16	76.2	10	2	ALL35_CYPDO	P81813 carcius ma
64	16	76.2	10	2	ALL36_CYPDO	P81813 carcius ma
65	16	76.2	10	2	ALL37_CYPDO	P81813 carcius ma
66	16	76.2	10	2	ALL38_CYPDO	P81813 carcius ma
67	16	76.2	10	2	ALL39_CYPDO	P81813 carcius ma
68	16	76.2	10	2	ALL40_CYPDO	P81813 carcius ma
69	16	76.2	10	2	ALL41_CYPDO	P81813 carcius ma
70	16	76.2	10	2	ALL42_CYPDO	P81813 carcius ma
71	16	76.2	10	2	ALL43_CYPDO	P81813 carcius ma
72	16	76.2	10	2	ALL44_CYPDO	P81813 carcius ma
73	16	76.2	10	2	ALL45_CYPDO	P81813 carcius ma
74	16	76.2	10	2	ALL46_CYPDO	P81813 carcius ma
75	16	76.2	10	2	ALL47_CYPDO	P81813 carcius ma
76	16	76.2	10	2	ALL48_CYPDO	P81813 carcius ma
77	16	76.2	10	2	ALL49_CYPDO	P81813 carcius ma
78	16	76.2	10	2	ALL50_CYPDO	P81813 carcius ma
79	16	76.2	10	2	ALL51_CYPDO	P81813 carcius ma
80	16	76.2	10	2	ALL52_CYPDO	P81813 carcius ma
81	16	76.2	10	2	ALL53_CYPDO	P81813 carcius ma
82	16	76.2	10	2	ALL54_CYPDO	P81813 carcius ma
83	16	76.2	10	2	ALL55_CYPDO	P81813 carcius ma
84	16	76.2	10	2	ALL56_CYPDO	P81813 carcius ma
85	16	76.2	10	2	ALL57_CYPDO	P81813 carcius ma
86	16	76.2	10	2	ALL58_CYPDO	P81813 carcius ma
87	16	76.2	10	2	ALL59_CYPDO	P81813 carcius ma
88	16	76.2	10	2	ALL60_CYPDO	P81813 carcius ma
89	16	76.2	10	2	ALL61_CYPDO	P81813 carcius ma
90	16	76.2	10	2	ALL62_CYPDO	P81813 carcius ma
91	16	76.2	10	2	ALL63_CYPDO	P81813 carcius ma
92	16	76.2	10	2	ALL64_CYPDO	P81813 carcius ma
93	16	76.2	10	2	ALL65_CYPDO	P81813 carcius ma
94	16	76.2	10	2	ALL66_CYPDO	P81813 carcius ma
95	16	76.2	10	2	ALL67_CYPDO	P81813 carcius ma
96	16	76.2	10	2	ALL68_CYPDO	P81813 carcius ma
97	16	76.2	10	2	ALL69_CYPDO	P81813 carcius ma
98	16	76.2	10	2	ALL70_CYPDO	P81813 carcius ma
99	16	76.2	10	2	ALL71_CYPDO	P81813 carcius ma
100	16	76.2	10	2	ALL72_CYPDO	P81813 carcius ma
101	16	76.2	10	2	ALL73_CYPDO	P81813 carcius ma
102	16	76.2	10	2	ALL74_CYPDO	P81813 carcius ma
103	16	76.2	10	2	ALL75_CYPDO	P81813 carcius ma
104	16	76.2	10	2	ALL76_CYPDO	P81813 carcius ma

105	12	57.1	9	2	Q7ZP3	Q7ZP3 human immun
106	12	57.1	9	2	Q7ZP5	Q7ZP5 human immun
107	12	57.1	9	2	Q7ZP7	Q7ZP7 human immun
108	12	57.1	9	2	Q7ZPK1	Q7ZPK1 human immun
109	12	57.1	10	1	CU30.LOCMI	CU30.LOCMI locusta mig
110	12	57.1	10	1	DYS2.LIMDU	DYS2.LIMDU limodysnae
111	12	57.1	10	1	DYS6.LIMSA	DYS6.LIMSA limodysnae
112	12	57.1	10	1	RT02.BOVIN	RT02.BOVIN limodysnae
113	12	57.1	10	1	TKU2.URGUN	TKU2.URGUN urochelis uni
114	12	57.1	10	1	Q7KZ59	Q7KZ59 homo sapien
115	12	57.1	10	2	Q25355	Q25355 locusta mig
116	12	57.1	10	2	Q25356	Q25356 locusta mig
117	12	57.1	10	2	Q85V65	Q85V65 eucalyptus
118	12	57.1	10	2	Q8SAC2	Q8SAC2 amblystegiu
119	12	57.1	10	2	Q7M111	Q7M111 phaseolus v
120	12	57.1	10	2	Q9S905	Q9S905 glycine max
121	12	57.1	10	2	Q9AE19	Q9AE19 streptococ
122	12	57.1	10	2	Q9R7J8	Q9R7J8 helicobacte
123	12	57.1	10	2	Q6LCT8	Q6LCT8 rattus norv
124	12	57.1	10	2	Q71VN2	Q71VN2 mus musculu
125	12	57.1	10	2	Q83978	Q83978 influenza a
126	12	57.1	10	2	Q8JFE7	Q8JFE7 ficedula al
127	12	57.1	10	2	Q8J333	Q8J333 ficedula hy
128	12	57.1	11	1	PVK1.BLACR	PVK1.BLACR blaberus cr
129	12	57.1	11	1	PVK1.BLADU	PVK1.BLADU blaptica du
130	12	57.1	11	1	PVK1.GROPO	PVK1.GROPO leucophaea
131	12	57.1	11	1	PVK1.LEUMA	PVK1.LEUMA nauphoeta c
132	12	57.1	11	1	PVK1.NAUCI	PVK1.NAUCI litoria rub
133	12	57.1	11	1	RE41.LITRU	RE41.LITRU homo sapien
134	12	57.1	11	2	Q9UC46	Q9UC46 litoria s
135	12	57.1	11	2	Q6UZ55	Q6UZ55 plasmodium
136	12	57.1	11	2	Q7RH63	Q7RH63 sus scrofa
137	12	57.1	11	2	Q9TRX0	Q9TRX0 oreochromis
138	12	57.1	11	2	Q7R871	Q7R871 oreochromis
139	12	57.1	11	2	Q7R872	Q7R872 oreochromis
140	12	57.1	11	2	Q7R873	Q7R873 oreochromis
141	12	57.1	11	2	Q34380	Q34380 drosophila
142	12	57.1	11	2	Q6RW44	Q6RW44 capsicum an
143	12	57.1	11	2	Q7M1A0	Q7M1A0 eubacterium
144	12	57.1	11	2	Q7M1D1	Q7M1D1 unidentified
145	12	57.1	11	2	Q9EUZ3	Q9EUZ3 escherichia
146	11	52.4	7	2	Q9CSB3	Q9CSB3 arbidopsis
147	11	52.4	8	1	CAD1.ENTFA	CAD1.ENTFA enterococcu
148	11	52.4	8	1	DYS4.LIMSA	DYS4.LIMSA limodysnae
149	11	52.4	8	1	DYS5.LIMSA	DYS5.LIMSA limodysnae
150	11	52.4	8	1	RT34.BOVIN	RT34.BOVIN bos taurus

## ALIGNMENTS

RESULT 1  
TKN4\_PSECU STANDARD; PRT; 11 AA.  
AC P42959;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Substance P-like peptide I (PG-SP1).  
OS Pseudophryne guentheri (Guenther's toadlet).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Myobatrachidae;  
OC Myobatrachinae; Pseudophryne.  
OX NCBI\_TaxID=30349;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Skin secretion;  
RX MEDLINE=90287814; PubMed=2356157; DOI=10.1016/0196-9781(90)90086-K;  
RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,  
RA Roberts J.D., Melchiorri P., Erspamer V.;  
RT "Six novel tachykinin- and bombesin-related peptides from the skin of  
RT the Australian frog Pseudophryne guentheri.",  
RL Peptides 11:299-304(1990).

CC -1- FUNCTION: Tachykinins are active peptides which excite neurons,  
CC evoke behavioral responses, are potent vasodilators and  
CC secretagogues, and contract (directly or indirectly) many smooth  
CC muscles.  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- TISSUE SPECIFICITY: Skin.  
CC -1- SIMILARITY: Belongs to the tachykinin family.  
DR PIR: E60409.  
DR InterPro: IPR002040; Tachy Neurokinin.  
DR InterPro: IPR008215; Tachykinin.  
DR Pfam: PF02202; Tachykinin; 1.  
DR SMART: SM00203; TK; 1.  
DR PROSITE: PS00267; TACHYKININ; 1.  
KW Amidation; Amphibian defense peptide; Direct protein sequencing;  
KW Neuropeptide; Pyrrolidone carboxylic acid; Tachykinin.  
FT MOD RES 1 1  
FT MOD RES 11 11  
FT MOD RES 11 11  
SQ SEQUENCE 11 AA; 1294 MW; 3A247C2CC9CB1A57 CRC64;

Query Match 100.0%; Score 21; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FGLM 4  
DB 8 FGLM 11

## RESULT 2

TKN5\_PSECU STANDARD; PRT; 11 AA.  
AC P42950;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Substance P-like peptide II (PG-SP1I).  
OS Pseudophryne guentheri (Guenther's toadlet).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Myobatrachidae;  
OC Myobatrachinae; Pseudophryne.  
OX NCBI\_TaxID=30349;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Skin secretion;  
RX MEDLINE=90287814; PubMed=2356157; DOI=10.1016/0196-9781(90)90086-K;  
RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,  
RA Roberts J.D., Melchiorri P., Erspamer V.;  
RT "Six novel tachykinin- and bombesin-related peptides from the skin of  
RT the Australian frog Pseudophryne guentheri.",  
RL Peptides 11:299-304(1990).  
CC -1- FUNCTION: Tachykinins are active peptides which excite neurons,  
CC evoke behavioral responses, are potent vasodilators and  
CC secretagogues, and contract (directly or indirectly) many smooth  
CC muscles.  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- TISSUE SPECIFICITY: Skin.  
CC -1- SIMILARITY: Belongs to the tachykinin family.  
DR PIR: F60409; F60409.  
DR InterPro: IPR002040; Tachy Neurokinin.  
DR Pfam: PF02202; Tachykinin; 1.  
DR PROSITE: PS00267; TACHYKININ; 1.  
KW Amidation; Amphibian defense peptide; Direct protein sequencing;  
KW Neuropeptide; Pyrrolidone carboxylic acid; Tachykinin.  
FT MOD RES 1 1  
FT MOD RES 11 11  
FT MOD RES 11 11  
SQ SEQUENCE 11 AA; 1293 MW; 3A247C2CC9CB1A57 CRC64;

Query Match 100.0%; Score 21; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FGLM 4  
DB 8 FGLM 11



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 26, 2005, 08:12:37 ; Search time 20.444 Seconds  
(without alignments)  
18.825 Million cell updates/sec

Title: UB-10-053-669-2  
Perfect score: 21  
Sequence: 1 FGLM 4

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 1328

Minimum DB seq length: 0  
Maximum DB seq length: 11

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 150 summaries

Database :  
1: p1r1:\*  
3: p1r2:\*  
4: p1r3:\*  
5: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21	100.0	11	1 A60654	substance P - guin
2	21	100.0	11	1 SPHO	substance P - hors
3	21	100.0	11	2 JN0023	substance P - chic
4	21	100.0	11	2 S33300	probable substance
5	21	100.0	11	2 E60409	substance P-like P
6	21	100.0	11	2 F60409	substance P-like P
7	21	100.0	11	2 S23308	substance P - rain
8	18	85.7	10	2 B49581	substance P - yel
9	18	85.7	10	2 A49581	substance P - yel
10	18	85.7	10	2 A24867	substance P - s
11	18	85.7	10	2 B61033	substance P - s
12	18	85.7	11	2 S07203	substance P - frog
13	18	85.7	11	2 S07201	substance P - frog
14	18	85.7	11	2 A61033	substance P - frog
15	18	85.7	11	2 D47353	substance P - frog
16	16	76.2	10	2 B60527	substance P - frog
17	16	76.2	10	2 B60589	substance P - frog
18	15	71.4	5	2 PT0278	substance P - frog
19	15	71.4	5	2 PT0278	substance P - frog
20	15	71.4	5	2 JN0024	substance P - frog
21	15	71.4	10	2 S06964	substance P - frog
22	15	71.4	10	2 S23307	substance P - frog
23	15	71.4	10	2 S23307	substance P - frog
24	15	71.4	10	2 S23307	substance P - frog
25	15	71.4	10	2 S07202	substance P - frog
26	15	71.4	10	2 C61033	substance P - frog
27	15	71.4	10	2 S27178	substance P - frog
28	15	71.4	11	1 E00CC	substance P - frog
29	15	71.4	11	1 E00CC	substance P - frog

30	15	71.4	11	2 C60409	kassinin-like pept
31	15	71.4	11	2 B60409	kassinin-like pept
32	15	71.4	11	2 B60409	kassinin-like pept
33	15	71.4	11	2 S23306	substance P - Acta
34	14	66.7	5	2 A44955	alkaloid monooxygen
35	14	66.7	8	2 B47393	neuropeptide calia
36	13	61.9	8	2 PC4373	telomeric and tetr
37	13	61.9	8	2 PC4373	telomeric and tetr
38	13	61.9	9	2 PT0225	substance P - Acta
39	13	61.9	9	2 PH1591	substance P - Acta
40	13	61.9	10	1 RHPCG	substance P - Acta
41	13	61.9	10	1 RHPCG	substance P - Acta
42	13	61.9	10	1 RHPCG	substance P - Acta
43	13	61.9	10	2 PT0230	substance P - Acta
44	13	61.9	10	2 PH1633	substance P - Acta
45	13	61.9	10	2 A59173	substance P - Acta
46	13	61.9	11	2 A57458	substance P - Acta
47	13	61.9	11	4 PC2124	substance P - Acta
48	12	57.1	7	1 A61324	substance P - Acta
49	12	57.1	7	2 S36662	substance P - Acta
50	12	57.1	7	2 A40504	substance P - Acta
51	12	57.1	8	2 PH0803	substance P - Acta
52	12	57.1	8	2 S11078	substance P - Acta
53	12	57.1	9	2 D24180	substance P - Acta
54	12	57.1	9	2 F28854	substance P - Acta
55	12	57.1	9	2 PH0942	substance P - Acta
56	12	57.1	9	2 G58502	substance P - Acta
57	12	57.1	9	2 PT0080	substance P - Acta
58	12	57.1	9	2 PC7074	substance P - Acta
59	12	57.1	9	2 S18850	substance P - Acta
60	12	57.1	10	2 PT0310	substance P - Acta
61	12	57.1	10	2 PH0807	substance P - Acta
62	12	57.1	10	2 S38305	substance P - Acta
63	12	57.1	11	2 PT0250	substance P - Acta
64	12	57.1	11	2 S57575	substance P - Acta
65	12	57.1	11	2 C58501	substance P - Acta
66	12	57.1	11	2 A44755	substance P - Acta
67	11	52.4	5	2 A61445	substance P - Acta
68	11	52.4	7	2 A60224	substance P - Acta
69	11	52.4	9	2 A11497	substance P - Acta
70	11	52.4	9	2 D44787	substance P - Acta
71	11	52.4	9	2 I49406	substance P - Acta
72	11	52.4	10	1 GMROL2	substance P - Acta
73	11	52.4	10	2 B60656	substance P - Acta
74	11	52.4	11	1 GMROL	substance P - Acta
75	11	52.4	11	2 A40593	substance P - Acta
76	11	52.4	11	2 PT0249	substance P - Acta
77	11	52.4	11	2 A60656	substance P - Acta
78	10	47.6	4	2 PT0240	substance P - Acta
79	10	47.6	4	2 A53284	substance P - Acta
80	10	47.6	5	2 A44817	substance P - Acta
81	10	47.6	5	2 I44817	substance P - Acta
82	10	47.6	5	2 E44817	substance P - Acta
83	10	47.6	5	2 A44817	substance P - Acta
84	10	47.6	5	2 A44817	substance P - Acta
85	10	47.6	6	2 B56979	substance P - Acta
86	10	47.6	6	2 PT0643	substance P - Acta
87	10	47.6	6	2 PT0718	substance P - Acta
88	10	47.6	6	2 PT0589	substance P - Acta
89	10	47.6	6	2 PT0727	substance P - Acta
90	10	47.6	7	2 PT0246	substance P - Acta
91	10	47.6	7	2 A11483	substance P - Acta
92	10	47.6	7	2 PT0663	substance P - Acta
93	10	47.6	7	2 T09512	substance P - Acta
94	10	47.6	7	2 S09066	substance P - Acta
95	10	47.6	7	2 PT0529	substance P - Acta
96	10	47.6	7	4 PC2056	substance P - Acta
97	10	47.6	7	4 PC2056	substance P - Acta
98	10	47.6	8	2 PA0032	substance P - Acta
99	10	47.6	8	2 PT0368	substance P - Acta
100	10	47.6	8	2 PT0627	substance P - Acta
101	10	47.6	8	2 PT0522	substance P - Acta
102	10	47.6	8	2 PT0559	substance P - Acta

103	10	47.6	8	2	PT0554	T-cell receptor be
104	10	47.6	8	2	PT0725	T-cell receptor be
105	10	47.6	8	2	PC4372	telomeric and tetr
106	10	47.6	8	2	A37521	R-phycocerythrin ga
107	10	47.6	8	2	F60588	sperm-activating p
108	10	47.6	8	2	E60588	sperm-activating p
109	10	47.6	8	2	G60588	sperm-activating p
110	10	47.6	8	4	IS5411	hypothetical histo
111	10	47.6	9	2	A61230	caldesquestrin, car
112	10	47.6	9	2	E28854	fibrinopeptide B -
113	10	47.6	9	2	D28854	fibrinopeptide B -
114	10	47.6	9	2	B33098	231k exantigen -
115	10	47.6	9	2	S65855	collagen alpha 2(V
116	10	47.6	9	2	PS0253	glycine cleavage s
117	10	47.6	9	2	A60356	118k stomach canc
118	10	47.6	9	2	S66635	alpha-2-macroglobu
119	10	47.6	10	1	ECLQJM	tachykinin I - mig
120	10	47.6	10	1	ECLQJM	tachykinin III - m
121	10	47.6	10	2	PN0136	pepsin IEC 3.4.23.
122	10	47.6	10	2	A60624	angiotensin I - Ja
123	10	47.6	10	2	SI0926	inhibin beta-A cha
124	10	47.6	10	2	C38925	seed storage prote
125	10	47.6	10	2	A35556	hypothetical prote
126	10	47.6	10	2	B24736	inhibin beta-B cha
127	10	47.6	10	2	S66214	cartilage oligomer
128	10	47.6	10	2	PT0632	T-cell receptor be
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130	10	47.6	10	2	S43630	cytochrome-c oxida
131	10	47.6	10	2	A90917	angiotensin precu
132	10	47.6	10	2	G60787	sperm-activating p
133	10	47.6	10	2	E60787	sperm-activating p
134	10	47.6	10	2	E60787	sperm-activating p
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136	10	47.6	10	2	B60588	sperm-activating p
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142	10	47.6	10	2	F60589	sperm-activating p
143	10	47.6	10	2	D60589	sperm-activating p
144	10	47.6	11	1	XASNBA	bradykinin-potentl
145	10	47.6	11	1	ECLQ2M	tachykinin II - ml
146	10	47.6	11	1	B58501	24k kidney and bla
147	10	47.6	11	2	S70720	trigger factor hom
148	10	47.6	11	2	I33098	173k exantigen -
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150	10	47.6	11	2		

## ALIGNMENTS

RESULT 1  
 A60654  
 Substance P - guinea pig  
 C/Species: Cavia porcellus (guinea pig)  
 C/Date: 14-May-1993 #sequence\_revision 27-Jun-1994 #text\_change 09-Jul-2004  
 C/Accession: A60654  
 R:Murphy, R.  
 Neuropeptides 14, 105-110, 1989  
 A/Title: Primary amino acid sequence of guinea-pig substance P.  
 A/Reference number: A60654; MUID:90044685; PMID:2478925  
 A/Accession: A60654  
 A/Molecule type: protein  
 A/Residues: 1-11 <MUR>  
 A/Cross-references: UNIPROT:P01290  
 C/Superfamily: substance P precursor  
 C/Keywords: amidated carboxyl end; neuropeptide; tachykinin  
 F/11/Modified site: amidated carboxyl end (Met) #status experimental

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 Best Local Similarity 100.0%; Pred. No. 19;

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RESULT 2  
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 Substance P - horse  
 C/Species: Equus caballus (domestic horse)  
 C/Date: 23-Oct-1981 #sequence\_revision 23-Oct-1981 #text\_change 09-Jul-2004  
 C/Accession: A01558  
 R/Studer, R.O.; Tizceciak, A.; Lergier, W.  
 Heiv. Chim. Acta 56, 860-866, 1973  
 A/Title: Isolierung und Aminosäuresequenz von Substanz P aus Pferdedarm.  
 A/Reference number: A01558  
 A/Accession: A01558  
 A/Molecule type: protein  
 A/Residues: 1-11 <STU>  
 A/Cross-references: UNIPROT:P01290  
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 Db 8 FGLM 11

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 Substance P - chicken  
 C/Species: Gallus gallus (chicken)  
 C/Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 09-Jul-2004  
 C/Accession: JN0023  
 R:Conlon, J.M.; Katsoulis, S.; Schmidt, W.E.; Thim, L.  
 Regul. Pept. 20, 171-180, 1988  
 A/Title: [Arg3]substance P and neurokinin A from chicken small intestine.  
 A/Reference number: JN0023; MUID:88204263; PMID:2452461  
 A/Accession: JN0023  
 A/Molecule type: protein  
 A/Residues: 1-11 <CON>  
 A/Cross-references: UNIPROT:P19850  
 C/Superfamily: substance P precursor  
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 F/11/Modified site: amidated carboxyl end (Met) #status predicted

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QY 1 FGLM 4  
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 Db 8 FGLM 11

RESULT 4  
 S33300  
 Probable substance P - smaller spotted catshark  
 C/Species: Scyliorhinus canicula (smaller spotted catshark, smaller spotted dogfish)  
 C/Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 09-Jul-2004  
 C/Accession: S33300  
 R:Wang, D.; Wang, Y.; Hazon, N.; Balmont, R.J.; Conlon, J.M.  
 Eur. J. Biochem. 214, 469-474, 1993  
 A/Title: Primary structures and biological activities of substance-P-related peptides fr  
 A/Reference number: S33300; MUID:93392508; PMID:7685693  
 A/Accession: S33300  
 A/Molecule type: protein

GenCore version 5.1.6  
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OM protein - protein search, using bw model

Run on: October 26, 2005, 08:13:37 ; Search time 96.444 Seconds  
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Title: US-10-053-669-2

Perfect score: 21  
Sequence: 1 FCIM 4

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Searched: 1862994 seqs, 417510619 residues

Total number of hits satisfying chosen parameters: 250346

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Post-processing: Minimum Match 0%

Maximum Match 100%

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Listing first 150 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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2	21	100.0	4	14 US-10-230-133-3	Sequence 3, Appli
3	21	100.0	4	14 US-10-053-669-2	Sequence 2, Appli
4	21	100.0	4	16 US-10-695-536-3	Sequence 3, Appli
5	21	100.0	4	16 US-10-805-881-2	Sequence 2, Appli
6	21	100.0	4	16 US-10-497-628-2	Sequence 2, Appli
7	21	100.0	4	19 US-11-018-690-3	Sequence 3, Appli
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; APPLICANT: Wellb, Ibert
; TITLE OF INVENTION: Method for Detecting Deficient Cellular Membrane Tightly Bound Mac
; FILE REFERENCE: 1427001
; CURRENT FILING DATE: 1999-03-10
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
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; ORGANISM: Homo sapiens
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; Publication No. US20030040625A1
; GENERAL INFORMATION:
; APPLICANT: Wellb, Ibert
; TITLE OF INVENTION: Antagonists of the magnesium binding defect as therapy agents and
; FILE REFERENCE: 2892-106
; CURRENT FILING DATE: 2002-08-29
; PRIOR FILING DATE: 2000-08-09
; NUMBER OF SEQ ID NOS: 4
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; ORGANISM: Homo sapiens
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; Sequence 2, Application US/10053669
; Publication No. US20030077658A1
; GENERAL INFORMATION:
; APPLICANT: Wellb, Ibert
; TITLE OF INVENTION: Method for Detecting Deficient Cellular Membrane Tightly Bound Mac
; FILE REFERENCE: N1427-005
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(without alignments)  
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Title: US-10-053-669-2  
Perfect score: 21  
Sequence: 1 FGLM 4

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 125705

Minimum DB seq length: 0  
Maximum DB-seq length: 11

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 150 summaries

Database :

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4: /cgnt2\_6/p/ptdata/1/1aa/6B\_COMB.pep:\*  
5: /cgnt2\_6/p/ptdata/1/1aa/PCTUS\_COMB.pep:\*  
6: /cgnt2\_6/p/ptdata/1/1aa/backfill1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	21	100.0	4	1	US-08-441-551-63 Sequence 63, Appl
2	21	100.0	4	1	US-08-303-362A-63 Sequence 63, Appl
3	21	100.0	4	3	US-09-265-690C-2 Sequence 2, Appl
4	21	100.0	4	4	US-09-635-266-3 Sequence 3, Appl
5	21	100.0	4	4	US-10-133-3 Sequence 3, Appl
6	21	100.0	4	5	PCT-US95-05600-80 Sequence 80, Appl
7	21	100.0	5	1	US-07-934-553-2 Sequence 2, Appl
8	21	100.0	5	1	US-08-225-474-2 Sequence 2, Appl
9	21	100.0	5	2	US-08-070-301-6 Sequence 6, Appl
10	21	100.0	5	2	US-07-737-371E-6 Sequence 6, Appl
11	21	100.0	5	3	US-07-737-371E-48 Sequence 48, Appl
12	21	100.0	5	2	US-09-265-690C-1 Sequence 1, Appl
13	21	100.0	6	1	US-07-934-553-3 Sequence 3, Appl
14	21	100.0	6	1	US-08-225-474-3 Sequence 3, Appl
15	21	100.0	6	1	US-08-430-238-15 Sequence 15, Appl
16	21	100.0	6	2	US-07-737-371E-5 Sequence 5, Appl
17	21	100.0	6	3	US-09-317-125-5 Sequence 3, Appl
18	21	100.0	6	4	US-09-428-692-39 Sequence 39, Appl
19	21	100.0	7	4	US-09-428-692-41 Sequence 41, Appl
20	21	100.0	7	1	US-07-712-828B-7 Sequence 7, Appl
21	21	100.0	7	2	US-07-737-371E-8 Sequence 8, Appl
22	21	100.0	8	2	US-09-428-692-42 Sequence 42, Appl
23	21	100.0	8	2	US-07-737-371E-10 Sequence 10, Appl
24	21	100.0	8	2	US-07-737-371E-56 Sequence 56, Appl
25	21	100.0	9	1	US-08-346-849-6 Sequence 6, Appl
26	21	100.0	9	2	US-07-737-371E-60 Sequence 6, Appl
27	21	100.0	9	2	US-08-293-284A-6 Sequence 6, Appl

28	21	100.0	9	4	US-08-898-300-6 Sequence 6, Appl
29	21	100.0	9	4	US-08-824-513-6 Sequence 6, Appl
30	21	100.0	10	1	US-08-088-322-6 Sequence 6, Appl
31	21	100.0	10	2	US-08-437-820-6 Sequence 6, Appl
32	21	100.0	10	2	US-07-737-371E-9 Sequence 9, Appl
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36	21	100.0	11	1	US-07-934-553-1 Sequence 1, Appl
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67	21	100.0	11	2	US-07-737-371E-18 Sequence 18, Appl
68	21	100.0	11	2	US-07-737-371E-19 Sequence 19, Appl
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70	21	100.0	11	2	US-07-737-371E-35 Sequence 35, Appl
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73	21	100.0	11	2	US-08-848-766A-1 Sequence 1, Appl
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84	21	100.0	11	4	US-09-629-642A-1 Sequence 1, Appl
85	21	100.0	11	4	US-10-230-133-1 Sequence 1, Appl
86	21	100.0	11	4	US-09-428-692-21 Sequence 21, Appl
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91	21	100.0	11	6	US-09-258-754-354 Sequence 354, App
92	21	100.0	8	3	US-09-042-107-354 Sequence 354, App
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95	18	85.7	8	4	US-08-021-623C-2 Sequence 2, Appl
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105 18 85.7 11 2 US-08-447-175A-7 Sequence 7, Appl1  
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126 16 76.2 5 4 US-09-886-135A-2 Sequence 2, Appl1  
127 16 76.2 5 4 US-10-337-105-3 Sequence 3, Appl1  
128 16 76.2 5 4 US-10-337-105-4 Sequence 4, Appl1  
129 16 76.2 6 3 US-09-196-93A-19 Sequence 19, Appl1  
130 16 76.2 7 1 US-07-822-275-3 Sequence 3, Appl1  
131 16 76.2 7 1 US-07-822-275-4 Sequence 4, Appl1  
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133 16 76.2 7 1 US-08-286-262-4 Sequence 4, Appl1  
134 16 76.2 7 2 US-08-548-974-12 Sequence 12, Appl1  
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136 16 76.2 7 4 US-09-274-454-12 Sequence 12, Appl1  
137 16 76.2 7 4 US-09-672-865-2 Sequence 2, Appl1  
138 16 76.2 8 1 US-08-522-326-4 Sequence 4, Appl1  
139 16 76.2 8 1 US-08-522-326-9 Sequence 9, Appl1  
140 16 76.2 8 1 US-08-522-326-10 Sequence 10, Appl1  
141 16 76.2 8 1 US-08-522-326-14 Sequence 14, Appl1  
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145 16 76.2 8 2 US-08-480-793-11 Sequence 11, Appl1  
146 16 76.2 8 3 US-09-420-211-12 Sequence 12, Appl1  
147 16 76.2 8 4 US-09-461-325-359 Sequence 359, Appl1  
148 16 76.2 8 4 US-10-012-542-359 Sequence 359, Appl1  
149 16 76.2 8 4 US-09-830-428A-14 Sequence 14, Appl1  
150 16 76.2 8 4 US-09-586-106D-181 Sequence 181, Appl1

## ALIGNMENTS

RESULT 1  
US-08-441-591-63  
Sequence 63, Application US/08441591  
Patent No. 5637682  
GENERAL INFORMATION:  
APPLICANT: NIEUWLANDT, D., GOLD, L. AND WECKER, M.  
TITLE OF INVENTION: HIGH-AFFINITY  
TITLE OF INVENTION: OLIGONUCLEOTIDE LIGANDS  
TITLE OF INVENTION: TO THE TACHYKININ  
TITLE OF INVENTION: SUBSTANCE P  
NUMBER OF SEQUENCES: 66  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Swanson & Bratschun, L.L.C.  
STREET: 8400 E. Prentice Avenue, Suite 200  
CITY: Englewood  
STATE: Colorado  
COUNTRY: USA  
ZIP: 80111

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MG storage  
COMPUTER: IBM compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/441,591  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION NUMBER: 08/303,362  
FILING DATE: 9-SEPTEMBER-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/714,131  
FILING DATE: 10-JUNE-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/931,473  
FILING DATE: 17-AUGUST-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/117,991  
FILING DATE: 8-SEPTEMBER 1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/536,428  
FILING DATE: 11-JUNE-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/964,624  
FILING DATE: 21-OCTOBER-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Barry J. Swanson  
REGISTRATION NUMBER: 33,215  
REFERENCE/DOCKET NUMBER: NEX21/C  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (303) 793-3333  
TELEFAX: (303) 793-3433  
INFORMATION FOR SEQ ID NO: 63:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-441-591-63  
Query Match 100.0%; Score 21; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 4.1e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 2  
US-08-303-362A-63  
Sequence 63, Application US/08303362A  
Patent No. 5648214  
GENERAL INFORMATION:  
APPLICANT: NIEUWLANDT, D., GOLD, L. AND WECKER, M.  
TITLE OF INVENTION: HIGH-AFFINITY  
TITLE OF INVENTION: OLIGONUCLEOTIDE LIGANDS  
TITLE OF INVENTION: TO THE TACHYKININ  
TITLE OF INVENTION: SUBSTANCE P  
NUMBER OF SEQUENCES: 66  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Swanson & Bratschun, L.L.C.  
STREET: 8400 E. Prentice Avenue, Suite 200  
CITY: Englewood  
STATE: Colorado  
COUNTRY: USA  
ZIP: 80111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MG storage  
COMPUTER: IBM compatible  
OPERATING SYSTEM: MS-DOS

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 26, 2005, 08:08:06 ; Search time 106.667 Seconds

(without alignments)

14,504 Million cell updates/sec

Title: US-10-053-669-2

Perfect score: 21

Sequence: 1 FGLM 4

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 494136

Minimum DB seq length: 0

Maximum DB seq length: 11

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

Database :

1: Genesep16Dec04:\*  
2: Genesep1990s:\*  
3: Genesep2000s:\*  
4: Genesep2001s:\*  
5: Genesep2002s:\*  
6: Genesep2003as:\*  
7: Genesep2003bs:\*  
8: Genesep2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	21	100.0	4	2	AAV31075 Non-cross
3	21	100.0	4	3	AAW33026 Human/rat
4	21	100.0	4	3	AAV67577 P antagon
5	21	100.0	4	4	AAW91447 Tachykin
6	21	100.0	4	5	ABBI10091 Substance
7	21	100.0	4	5	AAU77846 Tachykin
8	21	100.0	4	7	ADBE94198 High acti
9	21	100.0	4	8	ADR43772 Human mag
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12	21	100.0	5	2	AAW33007 Alpha-sub
13	21	100.0	5	2	AAW33010 Alpha-sub
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17	21	100.0	5	2	AAW54550 Cholecyst
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26	21	100.0	5	4	AAW54548 Cholecyst
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104	21	100.0	9	4	AAAG91369	Aag91369	Tachykini
105	21	100.0	9	4	AAB991348	Aag99148	Atypical
106	21	100.0	9	7	AAE338833	Aae38833	Membrane
107	21	100.0	9	7	ADP924528	Adi92528	Substance
108	21	100.0	9	8	ADDO4477	Ado04477	Substance
109	21	100.0	9	8	ADN95076	Adns5076	Mammalian
110	21	100.0	9	8	ADSI15335	Adsi15335	Substance
111	21	100.0	10	1	AAPO50633	Aap050633	Substance
112	21	100.0	10	2	AAE219333	Aar21933	Substance
113	21	100.0	10	2	AAE65181	Aar65181	S. cerevis
114	21	100.0	10	2	AAV99684	Aav99684	Substance
115	21	100.0	10	2	AAV06939	Aav06939	Substance
116	21	100.0	10	2	AAW92663	Aaw92663	Human tac
117	21	100.0	10	4	AAE66675	Aab66675	Tachykini
118	21	100.0	10	4	AAAB91445	Aab91445	Tachykini
119	21	100.0	10	4	AAAG93347	Aag99347	Atypical
120	21	100.0	10	4	AAAG64746	Aag64746	Substance
121	21	100.0	10	8	ADN12181	Adn12181	Amino aci
122	21	100.0	10	8	ADN27868	Adn27868	Trichomon
123	21	100.0	11	1	AAPE61480	Aap61480	Sequence
124	21	100.0	11	1	AAAP80312	Aap80312	Sequence
125	21	100.0	11	1	AAAR11854	Aar11854	Undecapep
126	21	100.0	11	2	AAAR3162	Aar3162	Stalic ac
127	21	100.0	11	2	AAAR28442	Aar28442	Substance
128	21	100.0	11	2	AAAR21969	Aar21969	Cyclic su
129	21	100.0	11	2	AAAR21942	Aar21942	Substance
130	21	100.0	11	2	AAAR21962	Aar21962	Substance
131	21	100.0	11	2	AAAR21945	Aar21945	Substance
132	21	100.0	11	2	AAAR21963	Aar21963	Substance
133	21	100.0	11	2	AAAR21949	Aar21949	Substance
134	21	100.0	11	2	AAAR21951	Aar21951	Substance
135	21	100.0	11	2	AAAR21934	Aar21934	Substance
136	21	100.0	11	2	AAAR21946	Aar21946	Substance
137	21	100.0	11	2	AAAR21964	Aar21964	Substance
138	21	100.0	11	2	AAAR21970	Aar21970	Cyclic su
139	21	100.0	11	2	AAAR21938	Aar21938	Substance
140	21	100.0	11	2	AAAR21941	Aar21941	Substance
141	21	100.0	11	2	AAAR21943	Aar21943	Substance
142	21	100.0	11	2	AAAR21954	Aar21954	Substance
143	21	100.0	11	2	AAAR2646	Aar2646	Neurokini
144	21	100.0	11	2	AAAR65243	Aar65243	Substance
145	21	100.0	11	2	AAAR77310	Aar77310	Substance
146	21	100.0	11	2	AAAW33181	Aaw33181	Mono-DTPA
147	21	100.0	11	2	AAAW33180	Aaw33180	Mono-DTPA
148	21	100.0	11	2	AAAW04616	Aaw04616	Substance
149	21	100.0	11	2	AAAW97975	Aaw97975	Substance
150	21	100.0	11	2	AAAW42973	Aaw42973	Substrate

## ALIGNMENTS

RESULT 1	
AAW41683	
ID	AAW41683 standard; peptide; 4 AA.
XX	
AC	AAW41683;
XX	
DT	09-JUN-1998 (first entry)
XX	
DE	Peptide used in ophthalmic drug to treat corneal disorders.
XX	
XX	
KW	Ophthalmic drug; corneal disorder; ulcer; epithelial peeling; dry eye;
KW	keratitis; insulin like growth factor-I; IGF-I; eye drop.
XX	
OS	Synthetic.
XX	
PH	
Key	Location/Qualifiers

FT	Modified-site	
FT		4
XX	/note= "C-terminal amide"	
XX		
FN	WO9749419-A1.	
XX		
PD	31-DEC-1997.	
XX		
PF	11-JUN-1997;	97WO-JP002015.
XX		
PR	26-JUN-1996;	96JP-00165612.
XX		
PA	(SANTEN ) SANTEN PHARM CO LTD.	
XX		
F1	Nishida T, Nakamura M, Nakata K;	
XX		
DR	WPI; 1998-076907/07.	
PT	Ophthalmic drug composition containing tetra:peptide - is useful as	
PT	corneal disorder remedy for corneal ulcer, corneal epithelial peeling,	
PT	dry eye, keratitis.	
XX		
PS	Claim 1; Page 15; 19pp; Japanese.	
XX		
CC	The present sequence represents a tetrapeptide which is the active	
CC	ingredient in an ophthalmic drug composition. It is used, together with	
CC	insulin like growth factor-I (IGF-I), to treat corneal disorders such as	
CC	corneal ulcer, corneal epithelial peeling, dry eye and keratitis. The	
CC	dosage is 0.1-5000 (preferably 1-1000) mg/day of the tetrapeptide and	
CC	0.001-100 (preferably 0.01-10) mg/day of IGF-I. The preferable form of	
CC	the composition is eye drops	
XX		
XX		
XQ	Sequence 4 AA;	

XX	AA31075 standard; peptide; 4 AA.
XX	AA31075
AC	AA31075;
DT	21-OCT-1999 (first entry)
XX	
DE	Non-crosslinked protein particle peptide 124.
XX	
KW	Non-crosslinked protein particle; diagnostic; therapy; monodisperse; albumin; haemoglobin; nanometer; micrometer; clearance.
XX	
OS	Synthetic.
XX	
FH	Key
FT	Modified-site            Location/Qualifiers 4
FT	/note= "C-terminal amide"
XX	
PN	US5945033-A.
PD	
XX	31-AUG-1999.
PF	
XX	12-NOV-1996;      96US-00747137.
PR	15-JAN-1991;      91US-00641720.
PR	13-OCT-1992;      92US-00959560.
PR	01-JUN-1993;      93US-00069831.
FR	14-MAR-1994;      94US-00212546.
PA	(HEMO-) HEMOSPHERE INC.



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OM protein - protein search, using sw model

Run on: October 26, 2005, 08:36:48 ; Search time 170 Seconds

(without alignments)  
15.061 Million cell updates/sec

Title: US-10-053-669-4  
Perfect score: 22  
Sequence: 1 FXGLM 5

Scoring table: BLOSUM62DX  
Gapop-10.0 ; Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 150 summaries

Database :

1: uniprot\_03:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	22	100.0	10	1	TKN1_SCYCA
2	22	100.0	10	1	TKNB_CHICK
3	22	100.0	10	1	TKNB_ONCMY
4	22	100.0	10	1	TKNB_RANCA
5	22	100.0	10	1	TKNB_RANRI
6	22	100.0	10	1	TKNC_RANCA
7	22	100.0	10	1	TKNC_PIG
8	22	100.0	10	1	TKNK_RANRI
9	22	100.0	10	1	TKN_EHARI
10	22	100.0	10	1	TKSI_AEDAE
11	22	100.0	10	1	TKS2_AEDAE
12	22	100.0	10	1	TKN1_PSEGU
13	22	100.0	10	1	TKN1_UPEIN
14	22	100.0	10	1	TKN1_UPERU
15	22	100.0	10	1	TKN2_PSEGU
16	22	100.0	10	1	TKN2_UPERU
17	22	100.0	10	1	TKN3_PSEGU
18	22	100.0	10	1	TKN4_PSEGU
19	22	100.0	10	1	TKN5_PSEGU
20	22	100.0	10	1	TKNA_CAVPO
21	22	100.0	10	1	TKNA_CHICK
22	22	100.0	10	1	TKNA_GADMO
23	22	100.0	10	1	TKNA_HORSE
24	22	100.0	10	1	TKNA_ONCMY
25	22	100.0	10	1	TKNA_RANCA
26	22	100.0	10	1	TKNA_RANRI
27	22	100.0	10	1	TKNA_SCYCA
28	22	100.0	10	1	TKN_ELECT
29	22	100.0	10	1	TKN_ELEMO
30	22	100.0	10	1	TKN_PHYFU
31	22	100.0	10	2	O9UAR8

32	22	100.0	12	1	TKN1_KASMA	P08613	kassina mac
33	22	100.0	12	1	TKN_KASSE	P08611	kassina sen
34	22	100.0	13	1	CPI_APLCA	Q10398	aplysia cal
35	22	100.0	14	1	TKNM_RANMA	P40951	rana margar
36	22	100.0	16	1	TKN1_TORMA	Q71248	torpedo mar
37	22	100.0	18	1	TKN2_SCYCA	P08609	scyllorhinu
38	22	100.0	21	1	TKNC_CARAU	P25421	carassius a
39	22	100.0	21	1	O9PRZ3	O9PRZ3	oncorhynch
40	22	100.0	21	2	O9PSJ1	O9PSJ1	alligator m
41	22	100.0	24	2	O9PRP3	O9PRP3	sphyrna lew
42	22	100.0	29	2	O673E3	O673E3	dehalococco
43	22	100.0	33	2	O8U5P2	O8U5P2	agrobacteri
44	22	100.0	35	2	O7UR55	O7UR55	rhodospirell
45	22	100.0	39	2	O832E2	O832E2	enterococcu
46	22	100.0	42	2	O62FX0	O62FX0	burkholderi
47	22	100.0	44	2	O9DDN3	O9DDN3	xenopus lae
48	22	100.0	45	2	O6LD93	O6LD93	rattus sp.
49	22	100.0	48	2	O9R820	O9R820	escherichia
50	22	100.0	50	2	O9A2N0	O9A2N0	bacterioph
51	22	100.0	50	2	O9CIA1	O9CIA1	lactococcus
52	22	100.0	54	2	O9PGV0	O9PGV0	xyella fas
53	22	100.0	58	2	O89HU8	O89HU8	bradyrhizob
54	22	100.0	59	2	O6KGL7	O6KGL7	bacterioph
55	22	100.0	61	2	O9T5S8	O9T5S8	bos taurus
56	22	100.0	61	2	O6MD93	O6MD93	parachlamyd
57	22	100.0	61	2	O89463	O89463	heliobacter
58	22	100.0	63	2	O884T4	O884T4	pseudomonas
59	22	100.0	65	2	O7R2K1	O7R2K1	neurospora
60	22	100.0	67	2	O19443	O19443	caenorhabdi
61	22	100.0	69	1	YAT1_RHOBL	YAT1_RHOBL	rhodospseudo
62	22	100.0	69	2	O9CJ49	O9CJ49	lactococcus
63	22	100.0	69	2	O6ME20	O6ME20	parachlamyd
64	22	100.0	69	2	O8JXW0	O8JXW0	virus phich
65	22	100.0	70	2	O94JCS	O94JCS	oryza sativ
66	22	100.0	70	2	O8XWK6	O8XWK6	rateltonia s
67	22	100.0	72	2	O9Y494	O9Y494	homo sapien
68	22	100.0	74	2	O8IWZ7	O8IWZ7	homo sapien
69	22	100.0	76	2	O86UJ6	O86UJ6	homo sapien
70	22	100.0	76	2	O632P9	O632P9	bacillus ce
71	22	100.0	76	2	O72YS5	O72YS5	bacillus ce
72	22	100.0	76	2	O81KE4	O81KE4	bacillus an
73	22	100.0	78	2	O6HC90	O6HC90	bacillus th
74	22	100.0	78	2	O20445	O20445	limulus pol
75	22	100.0	79	2	O35733	O35733	rattus norv
76	22	100.0	80	2	O931B7	O931B7	staphylococ
77	22	100.0	82	2	O6BCK5	O6BCK5	oryctolagus
78	22	100.0	82	2	O98SD3	O98SD3	gulliaridia
79	22	100.0	84	1	ATPL_THIFE	P41173	thiobacilli
80	22	100.0	84	2	O6YME5	O6YME5	cacopsylla
81	22	100.0	84	2	O6YME9	O6YME9	arycinnis b
82	22	100.0	84	2	O6YME7	O6YME7	arycinnis h
83	22	100.0	84	2	O6YMF1	O6YMF1	arycinnis g
84	22	100.0	84	2	O6YMF5	O6YMF5	arycinnis o
85	22	100.0	84	2	O6YMF7	O6YMF7	arycinnis c
86	22	100.0	84	2	O6YMG1	O6YMG1	arycinnis m
87	22	100.0	84	2	O6YMG3	O6YMG3	arycinnis f
88	22	100.0	84	2	O6YMG5	O6YMG5	arycinnis r
89	22	100.0	84	2	O6YMH7	O6YMH7	arycinnis u
90	22	100.0	84	2	O6YMH7	O6YMH7	arycinnis n
91	22	100.0	84	2	O6YMK3	O6YMK3	arycinnis m
92	22	100.0	84	2	O6YMK7	O6YMK7	arycinnis m
93	22	100.0	84	2	O6YML9	O6YML9	arycinnis d
94	22	100.0	84	2	O6YMM1	O6YMM1	arycinnis d
95	22	100.0	84	2	O6YMM3	O6YMM3	arycinnis d
96	22	100.0	84	2	O6YMM5	O6YMM5	arycinnis d
97	22	100.0	84	2	O6YMM3	O6YMM3	arycinnis c
98	22	100.0	84	2	O6YMO5	O6YMO5	arycinnis ad
99	22	100.0	85	2	O9TW63	O9TW63	aedes aegypt
100	22	100.0	85	2	O9UAR7	O9UAR7	aedes aegypt
101	22	100.0	85	2	O6YMU1	O6YMU1	arycinnis p
102	22	100.0	86	2	O6F1O3	O6F1O3	mesoplasma
103	22	100.0	86	2	O9P233	O9P233	xeestia c-n1
104	22	100.0	87	1	TKN1_OCTVU	O91663	octopus vul

105	22	100.0	87	2	Q86UJ7	Q86UJ7 homo sapien
106	22	100.0	87	2	Q6YMB9	Q6YMB9 livilla com
107	22	100.0	87	2	Q6YMC1	Q6YMC1 livilla bae
108	22	100.0	87	2	Q6YMC3	Q6YMC3 livilla cap
109	22	100.0	87	2	Q6YMC9	Q6YMC9 livilla mon
110	22	100.0	87	2	Q6YMD1	Q6YMD1 livilla mon
111	22	100.0	87	2	Q6YMD3	Q6YMD3 livilla mon
112	22	100.0	87	2	Q6YMD5	Q6YMD5 livilla mau
113	22	100.0	87	2	Q6YMD7	Q6YMD7 livilla bla
114	22	100.0	87	2	Q6YMD9	Q6YMD9 livilla adu
115	22	100.0	87	2	Q6YME1	Q6YME1 cyamophila
116	22	100.0	87	2	Q6YME3	Q6YME3 cacopsylla
117	22	100.0	87	2	Q6YMF3	Q6YMF3 arctimlis o
118	22	100.0	87	2	Q6YMG7	Q6YMG7 arctainilla
119	22	100.0	87	2	Q6YMH5	Q6YMH5 arctainilla
120	22	100.0	87	2	Q6YMI3	Q6YMI3 arctainilla
121	22	100.0	87	2	Q6YMA9	Q6YMA9 arctimlis n
122	22	100.0	87	2	Q6YMA1	Q6YMA1 arctainilla
123	22	100.0	87	2	Q6YMA5	Q6YMA5 arctaina vi
124	22	100.0	87	2	Q6YMA7	Q6YMA7 arctaina nu
125	22	100.0	87	2	Q6YMQ3	Q6YMQ3 arctaina ad
126	22	100.0	87	2	Q6YMQ7	Q6YMQ7 arctaina ad
127	22	100.0	87	2	Q6YMQ9	Q6YMQ9 acizzia unc
128	22	100.0	87	2	Q6YMR1	Q6YMR1 acizzia hol
129	22	100.0	87	2	Q6YMY3	Q6YMY3 euhadra qua
130	22	100.0	89	2	Q8LMB5	Q8LMB5 oryza baciv
131	22	100.0	92	1	TKN2 OCTVU	Q81682 octopus vul
132	22	100.0	92	2	Q6AL16	Q6AL16 desulfoacte
133	22	100.0	93	1	Y011_MYCBO	Y011_MYCBO mycobacteri
134	22	100.0	93	1	Y011_MYCTU	Y011_MYCTU mycobacteri
135	22	100.0	93	1	Y013_MYCLE	Y013_MYCLE mycobacteri
136	22	100.0	93	2	Q6J2W7	Q6J2W7 boletinelu
137	22	100.0	93	2	Q744R9	Q744R9 mycobacteri
138	22	100.0	94	2	Q82PD5	Q82PD5 streptomyce
139	22	100.0	95	2	Q9Y6T4	Q9Y6T4 homo sapien
140	22	100.0	96	1	YNEC_ECO57	YNEC_ECO57 escherichia
141	22	100.0	96	1	YNEC_ECOLI	YNEC_ECOLI escherichia
142	22	100.0	96	2	Q86UJ8	Q86UJ8 homo sapien
143	22	100.0	96	2	Q66E24	Q66E24 yerisnia ps
144	22	100.0	96	2	Q74PW0	Q74PW0 yerisnia pe
145	22	100.0	96	2	Q82IT1	Q82IT1 yerisnia pe
146	22	100.0	96	2	Q83L16	Q83L16 shigella fl
147	22	100.0	97	2	Q8ND57	Q8ND57 homo sapien
148	22	100.0	97	2	Q6AB45	Q6AB45 propionibac
149	22	100.0	98	2	Q7YCY0	Q7YCY0 sarcophaga
150	22	100.0	99	2	Q9MLP9	Q9MLP9 limulus pol

## ALIGNMENTS

RESULT 1  
TKN1\_SCYCA STANDARD; PRT; 10 AA.  
AC P08608;  
DT 01-AUG-1988 (Rel. 08, Created)  
DT 01-AUG-1988 (Rel. 08, Last sequence update)  
DT 05-JUN-2004 (Rel. 44, Last annotation update)  
DE Scyllorhynchus I.  
OS Scyllorhynchus canicula (Spotted dogfish) (Spotted catshark).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;  
OC Elasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes;  
OC Scyllorhinidae; Scyllorhinus.  
NCBI\_TaxID=7830;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Intestine; PubMed=2422058; DOI=10.1016/0014-5793(86)80521-X;  
RX MEDLINE=86192829; Pubmed=2422058; DOI=10.1016/0014-5793(86)80521-X;  
RA Conlon J.M., Deacon C.F., O'Toole L., Thim L.;  
RT "Scyllorhynchus I and II: two novel tachykinins from dogfish gut."  
RL FEBS Lett. 200:111-116(1986).  
RN [2]  
RP SEQUENCE.

RC TISSUE=Brain; PubMed=7685693;  
RX MEDLINE=93292508; Pubmed=7685693;  
RA Maugh D., Wang Y., Hazon N., Balmert R.J., Conlon J.M.;  
RT "Primary structures and biological activities of substance-P-related peptides from the brain of the dogfish, Scyllorhynchus canicula."  
RL Eur. J. Biochem. 214:469-474(1993).  
CC -1- FUNCTION: Tachykinins are active peptides which excite neurons, evoke behavioral responses, are potent vasodilators and secreteagogues, and contract (directly or indirectly) many smooth muscles.  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- SIMILARITY: Belongs to the tachykinin family.  
DR PIR; A24867; A24867.  
DR InterPro; IPR002040; Tachy\_Neurokinin.  
DR PROSITE; PS00267; TACHYKININ; 1.  
KW Amidation; Direct protein sequencing; Neuropeptide; Tachykinin.  
FT MOD\_RES 10 Methionine amide.  
SQ SEQUENCE 10 AA; 1219 MW; D0602D6B59C33AA9 CRC64;

Query Match 100.0%; Score 22; DB 1; Length 10;  
Best Local Similarity 80.0%; Pred. No. 1.4e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXGLM 5  
|:|:|  
Db 6 FXGLM 10

RESULT 2  
TKNB\_CHICK STANDARD; PRT; 10 AA.  
AC P19851;  
DT 01-FEB-1991 (Rel. 17, Created)  
DT 01-FEB-1991 (Rel. 17, Last sequence update)  
DT 25-OCT-2004 (Rel. 45, Last annotation update)  
DE Neurokinin A (Substance K) (Neuromedin L).  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
OC Gallus.

NCBI\_TaxID=9031;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Intestine; PubMed=2452461; DOI=10.1016/0167-0115(88)90050-X;  
RX MEDLINE=88204263; Pubmed=2452461; DOI=10.1016/0167-0115(88)90050-X;  
RA Conlon J.M., Katsoulis S., Schmidt W.E., Thim L.;  
RT " [Arg3]substance P and neurokinin A from chicken small intestine.";  
RL Regul. Pept. 20:171-180(1988).  
CC -1- FUNCTION: Tachykinins are active peptides which excite neurons, evoke behavioral responses, are potent vasodilators and secreteagogues, and contract (directly or indirectly) many smooth muscles.  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- SIMILARITY: Belongs to the tachykinin family.  
DR PIR; UN0024; UN0024.  
DR PDB; 1NET; NMR; A=1-10.  
DR InterPro; IPR002040; Tachy\_Neurokinin.  
DR Pfam; PF02202; Tachykinin; 1.  
DR PROSITE; PS00267; TACHYKININ; 1.  
KW 3D-structure; Amidation; Direct protein sequencing; Neuropeptide; Tachykinin.  
FT MOD\_RES 10 Methionine amide.  
SQ SEQUENCE 10 AA; 1134 MW; 8A6B4062C9DBAB1 CRC64;

Query Match 100.0%; Score 22; DB 1; Length 10;  
Best Local Similarity 80.0%; Pred. No. 1.4e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 FXGLM 5  
|:|:|  
Db 6 FXGLM 10

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OM protein - protein search, using sw model

Run on: October 26, 2005, 08:37:28 ; Search time 39 Seconds  
(without alignments)  
12.335 Million cell updates/sec

Title: US-10-053-669-4  
Perfect score: 22  
Sequence: 1 FXGLM 5

Scoring table: BLOSUM62DX  
Gapop 10.0, Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB-seq length: 0  
Maximum DB-seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 150 summaries

Database:

PIR 79:\*  
1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	22	100.0	10	1 SPBGNK	neurokinin K - pig
2	22	100.0	10	2 JN0024	neurokinin A - chi
3	22	100.0	10	2 B49581	scylorhynchin II - ye
4	22	100.0	10	2 A49581	scylorhynchin I - ye
5	22	100.0	10	2 A49581	scylorhynchin I - s
6	22	100.0	10	2 S23307	neurokinin A - ral
7	22	100.0	10	2 S23386	neurokinin A - Acl
8	22	100.0	10	2 S07282	phyllomedulin - tw
9	22	100.0	10	2 C61033	ranatetachykinin C -
10	22	100.0	10	2 B61033	ranatetachykinin B -
11	22	100.0	10	2 S27178	neurokinin A-relat
12	22	100.0	11	1 A60654	substance P - guin
13	22	100.0	11	1 EOCC	eledoisin - musky
14	22	100.0	11	1 EOCC	eledoisin - curled
15	22	100.0	11	1 SPHO	substance P - hors
16	22	100.0	11	2 JN0023	substance P - chic
17	22	100.0	11	2 S33300	probable substance
18	22	100.0	11	2 S07203	urotelin - frog (
19	22	100.0	11	2 C60409	kaasainin-like pept
20	22	100.0	11	2 B60409	substance P-like P
21	22	100.0	11	2 B60409	kaasainin-like pept
22	22	100.0	11	2 F60409	substance P-like P
23	22	100.0	11	2 D60409	kaasainin-like pept
24	22	100.0	11	2 S23308	substance P - rain
25	22	100.0	11	2 S23306	substance P - Atla
26	22	100.0	11	2 S07201	physalaemin - frog
27	22	100.0	11	2 A61033	ranatetachykinin A -
28	22	100.0	12	2 S10059	tachykinin - Afric
29	22	100.0	12	2 S07206	kaasainin - Senegal

30	22	100.0	16	2 A60839	neurokinin A homo
31	22	100.0	18	2 B24867	scylorhynchin II -
32	22	100.0	21	2 JH0361	carasinin - goldfis
33	22	100.0	33	2 F97371	hypothetical prote
34	22	100.0	50	2 A86583	prophage p11 prote
35	22	100.0	54	2 C82836	hypothetical prote
36	22	100.0	63	2 UC2412	tachykinin gamma c
37	22	100.0	67	2 T16071	hypothetical prote
38	22	100.0	69	2 E86644	hypothetical prote
39	22	100.0	69	2 S04666	hypothetical prote
40	22	100.0	72	2 JC5455	preprotachykinin-A
41	22	100.0	72	2 T62742	tachykinin A gamma
42	22	100.0	80	2 S13840	hypothetical prote
43	22	100.0	82	2 E90119	40S ribosomal prot
44	22	100.0	93	2 E86910	conserved hypothet
45	22	100.0	93	2 A70659	hypothetical prote
46	22	100.0	96	2 E90894	hypothetical prote
47	22	100.0	96	2 D85723	hypothetical prote
48	22	100.0	96	2 AF0050	conserved hypothet
49	22	100.0	96	2 A64906	hypothetical prote
50	22	100.0	97	2 S12958	tachykinin delta P
51	22	100.0	99	2 S14586	Ig lambda chain V
52	22	100.0	102	2 F90997	probable minor tai
53	22	100.0	102	2 E85817	probable minor tai
54	22	100.0	102	2 T17741	hypothetical prote
55	22	100.0	102	2 AB0101	hypothetical prote
56	22	100.0	103	2 S28823	transcription fact
57	22	100.0	103	2 D49852	hypothetical prote
58	22	100.0	104	2 F87731	protein W10C8.2 [i
59	22	100.0	105	2 JE0384	NADH2 dehydrogenas
60	22	100.0	109	2 AF0940	conserved hypothet
61	22	100.0	112	1 SPRTA	substance P alpha
62	22	100.0	115	1 SPB8G	substance P gamma
63	22	100.0	115	2 S47039	tachykinin 1 precu
64	22	100.0	116	2 T65342	tachykinin B precu
65	22	100.0	116	2 A43179	neurokinin B precu
66	22	100.0	116	2 C72232	hypothetical prote
67	22	100.0	118	1 IECC5B	hypothetical prote
68	22	100.0	121	2 C42573	NADH2 dehydrogenas
69	22	100.0	122	2 T09187	hypothetical prote
70	22	100.0	123	2 B69050	conserved hypothet
71	22	100.0	124	2 B86771	hypothetical prote
72	22	100.0	126	2 T63117	cytochrome-c oxida
73	22	100.0	126	2 T63117	cytochrome-c oxida
74	22	100.0	126	2 A25905	tachykinin B precu
75	22	100.0	129	1 SPB8B	neurokinin 1 precu
76	22	100.0	130	1 SPB8B	neurokinin 1 precu
77	22	100.0	130	1 SPRTB	substance P beta P
78	22	100.0	130	2 S47038	tachykinin 1 precu
79	22	100.0	130	2 T52526	neurokinin 1 precu
80	22	100.0	131	2 A53024	leidyg insulin-lik
81	22	100.0	133	2 B89869	enterotoxin Yent1
82	22	100.0	135	2 T17787	hypothetical prote
83	22	100.0	136	2 AG2021	hypothetical prote
84	22	100.0	137	2 G90899	probable minor tai
85	22	100.0	145	2 F97328	hypothetical prote
86	22	100.0	154	2 S76409	hypothetical prote
87	22	100.0	159	2 B71046	hypothetical prote
88	22	100.0	161	2 A39624	5-11poxygenase-act
89	22	100.0	161	2 JC2402	FMS7 homolog m1sma
90	22	100.0	161	2 S08206	5-11poxygenase-act
91	22	100.0	163	2 H97417	probable two-compo
92	22	100.0	166	2 AG1931	hypothetical prote
93	22	100.0	172	1 DEMS6	NADH2 dehydrogenas
94	22	100.0	172	1 DERTN6	NADH2 dehydrogenas
95	22	100.0	173	2 T11348	NADH2 dehydrogenas
96	22	100.0	173	2 E83931	hypothetical prote
97	22	100.0	173	2 S65999	streptochicline ac
98	22	100.0	174	2 T11491	NADH2 dehydrogenas
99	22	100.0	174	2 T11400	NADH2 dehydrogenas
100	22	100.0	174	2 D82629	hypothetical prote
101	22	100.0	175	1 DEBON6	NADH2 dehydrogenas
102	22	100.0	175	2 T11504	NADH2 dehydrogenas

103	22	100.0	175	2	T11452	NADH2 dehydrogenas
104	22	100.0	175	2	T11451	NADH2 dehydrogenas
105	22	100.0	175	2	T1143	NADH2 dehydrogenas
106	22	100.0	175	2	S41846	NADH2 dehydrogenas
107	22	100.0	175	2	S26162	NADH2 dehydrogenas
108	22	100.0	175	2	D58851	NADH2 dehydrogenas
109	22	100.0	175	2	S41831	NADH2 dehydrogenas
110	22	100.0	175	2	T11374	NADH2 dehydrogenas
111	22	100.0	175	2	T11868	NADH2 dehydrogenas
112	22	100.0	175	2	T11258	NADH2 dehydrogenas
113	22	100.0	175	2	T10983	NADH2 dehydrogenas
114	22	100.0	175	2	T11061	NADH2 dehydrogenas
115	22	100.0	176	2	S02210	con-8 protein - Ne
116	22	100.0	178	2	T48711	hypothetical prote
117	22	100.0	180	2	F87358	hypothetical prote
118	22	100.0	181	2	F81851	hypothetical prote
119	22	100.0	184	2	S74741	hypothetical prote
120	22	100.0	184	2	E90077	conserved hypotet
121	22	100.0	187	2	T02887	probable calmodul
122	22	100.0	187	2	AF3009	hypothetical prote
123	22	100.0	191	2	AE2135	hypothetical prote
124	22	100.0	193	2	T26510	hypothetical prote
125	22	100.0	195	2	H98274	hypothetical prote
126	22	100.0	197	2	T36696	probable regulator
127	22	100.0	198	2	AF1870	hypothetical prote
128	22	100.0	199	2	S73702	hypothetical prote
129	22	100.0	200	1	A39741	cytochrome c bioge
130	22	100.0	203	2	B90055	hypothetical prote
131	22	100.0	205	2	T08398	calmodulin homolog
132	22	100.0	208	2	T08452	hypothetical prote
133	22	100.0	210	2	D97502	hypothetical prote
134	22	100.0	210	2	AH2720	RhtB family transp
135	22	100.0	210	2	T28002	hypothetical prote
136	22	100.0	210	2	AD2818	conserved hypotet
137	22	100.0	211	1	ICMS6	interleukin-6 prec
138	22	100.0	211	2	A34247	interleukin-6 prec
139	22	100.0	211	2	D69529	conserved hypotet
140	22	100.0	215	2	JX0244	pyroglutamy1-pepti
141	22	100.0	215	2	S23432	two component resp
142	22	100.0	216	2	A12635	prostaglandin B2 r
143	22	100.0	217	2	D53216	conserved hypotet
144	22	100.0	219	2	F69341	serine acetyltrans
145	22	100.0	220	2	D72349	conserved hypotet
146	22	100.0	223	2	D82210	conserved hypotet
147	22	100.0	223	2	E90392	hypothetical prote
148	22	100.0	228	2	E86253	hypothetical prote
149	22	100.0	229	2	E71010	hypothetical prote
150	22	100.0	230	1	H64634	conserved hypotet

## ALIGNMENTS

RESULT 1  
SPPCNK  
neuromedin K - pig  
C/Species: Sus scrofa domestica (domestic pig)  
C/Date: 19-Feb-1984 #sequence\_revision 19-Feb-1984 #text\_change 09-Jul-2004  
C/Accession: A01560  
R/Kangawa, K.; Minamino, N.; Fukuda, A.; Matsuo, H.  
Biochem. Biophys. Res. Commun. 114, 533-540, 1983  
A/Title: Neuromedin K: a novel mammalian tachykinin identified in porcine spinal cord.  
A/Reference number: A01560; PMID:83282812; PMID:6576785  
A/Accession: A01560  
A/Molecule type: protein  
A/Residues: 1-10 <KAN>  
A/Cross-references: UNIPROT:P01292  
A/Note: the structure of the peptide was confirmed by synthesis  
C/Comment: The biological source of this peptide is spinal cord. It stimulates smooth mu  
C/Superfamily: neurokinin B precursor  
C/Keywords: amidated carboxyl end; homone; spinal cord  
P/10/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 100.0%; Score 22; DB 1; Length 10;  
Best Local Similarity 80.0%; Pred. No. 21;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 FXGLM 5  
Db 6 FVGLM 10

RESULT 2  
JN0024  
neurokinin A - chicken  
C/Species: Gallus gallus (chicken)  
C/Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 09-Jul-2004  
C/Accession: JN0024  
R/Conlon, J.M.; Karsouls, S.; Schmidt, W.E.; Thim, L.  
Regul. Pept. 20, 171-180, 1988  
A/Title: [Arg3]substance P and neurokinin A from chicken small intestine.  
A/Reference number: JN0023; PMID:88204263; PMID:2452461  
A/Accession: JN0024  
A/Molecule type: protein  
A/Residues: 1-10 <CON>  
A/Cross-references: UNIPROT:P19851  
C/Superfamily: Substance P precursor  
C/Keywords: amidated carboxyl end; neuropeptide; tachykinin  
F/10/Modified site: amidated carboxyl end (Met) #status predicted

Query Match 100.0%; Score 22; DB 2; Length 10;  
Best Local Similarity 80.0%; Pred. No. 21;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 FXGLM 5  
Db 6 FVGLM 10

RESULT 3  
B49581  
sialokinin II - yellow fever mosquito  
C/Species: Aedes aegypti (yellow fever mosquito)  
C/Date: 06-Oct-1994 #sequence\_revision 18-Nov-1994 #text\_change 16-Aug-2004  
C/Accession: B49581  
R/Champagne, D.E.; Ribeiro, J.M.  
Proc. Natl. Acad. Sci. U.S.A. 91, 138-142, 1994  
A/Title: Sialokinin I and II: vasodilatory tachykinins from the yellow fever mosquito Aek  
A/Reference number: A49581; PMID:94105119; PMID:8278354  
A/Accession: B49581  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-10 <CHA>  
A/Cross-references: UNIPROT:P42635  
A/Experimental source: Rockefeller, salivary gland  
A/Note: sequence extracted from NCBI backbone (NCBIP:141842)

Query Match 100.0%; Score 22; DB 2; Length 10;  
Best Local Similarity 80.0%; Pred. No. 21;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 FXGLM 5  
Db 6 FVGLM 10

RESULT 4  
A49581  
sialokinin I - yellow fever mosquito  
C/Species: Aedes aegypti (yellow fever mosquito)  
C/Date: 06-Oct-1994 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004  
C/Accession: A49581  
R/Champagne, D.E.; Ribeiro, J.M.  
Proc. Natl. Acad. Sci. U.S.A. 91, 138-142, 1994  
A/Title: Sialokinin I and II: vasodilatory tachykinins from the yellow fever mosquito Aek  
A/Reference number: A49581; PMID:94105119; PMID:8278354

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 26, 2005, 08:40:49 ; Search time 166 Seconds  
(without alignments)  
12.576 Million cell updates/sec

Title: US-10-053-669-4  
Perfect score: 1 FXGLM 5  
Sequence: 1

Scoring table: BLOSUM62DX  
Gapop 10.0 , Gapext 0.5

Searched: 1862994 seqs, 417510619 residues

Total number of hits satisfying chosen parameters: 1862994

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 150 summaries

Database: Published Applications AA\*  
1: /cgn2\_6/prodata/1/pubppa/US07\_PUBCOMB.pep:\*  
2: /cgn2\_6/prodata/1/pubppa/PCR\_NEW\_PUB.pep:\*  
3: /cgn2\_6/prodata/1/pubppa/US06\_NEW\_PUB.pep:\*  
4: /cgn2\_6/prodata/1/pubppa/US06\_PUBCOMB.pep:\*  
5: /cgn2\_6/prodata/1/pubppa/US07\_NEW\_PUB.pep:\*  
6: /cgn2\_6/prodata/1/pubppa/PCRUS\_PUBCOMB.pep:\*  
7: /cgn2\_6/prodata/1/pubppa/US08\_NEW\_PUB.pep:\*  
8: /cgn2\_6/prodata/1/pubppa/US09\_PUBCOMB.pep:\*  
9: /cgn2\_6/prodata/1/pubppa/US09\_PUBCOMB.pep:\*  
10: /cgn2\_6/prodata/1/pubppa/US09\_PUBCOMB.pep:\*  
11: /cgn2\_6/prodata/1/pubppa/US09\_PUBCOMB.pep:\*  
12: /cgn2\_6/prodata/1/pubppa/US09\_NEW\_PUB.pep:\*  
13: /cgn2\_6/prodata/1/pubppa/US10\_PUBCOMB.pep:\*  
14: /cgn2\_6/prodata/1/pubppa/US10\_PUBCOMB.pep:\*  
15: /cgn2\_6/prodata/1/pubppa/US10\_PUBCOMB.pep:\*  
16: /cgn2\_6/prodata/1/pubppa/US10\_PUBCOMB.pep:\*  
17: /cgn2\_6/prodata/1/pubppa/US10\_PUBCOMB.pep:\*  
18: /cgn2\_6/prodata/1/pubppa/US10\_NEW\_PUB.pep:\*  
19: /cgn2\_6/prodata/1/pubppa/US11\_PUBCOMB.pep:\*  
20: /cgn2\_6/prodata/1/pubppa/US11\_NEW\_PUB.pep:\*  
21: /cgn2\_6/prodata/1/pubppa/US60\_NEW\_PUB.pep:\*  
22: /cgn2\_6/prodata/1/pubppa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	22	100.0	5	9	US-09-265-690C-1
2	22	100.0	5	9	US-09-265-690C-4
3	22	100.0	5	14	US-10-230-133-4
4	22	100.0	5	14	US-10-053-669-1
5	22	100.0	5	14	US-10-053-669-4
6	22	100.0	5	15	US-10-134-187-3
7	22	100.0	5	16	US-10-688-741-3
8	22	100.0	5	16	US-10-695-536-4
9	22	100.0	5	16	US-10-805-881-1
10	22	100.0	5	16	US-10-805-881-4
11	22	100.0	5	16	US-10-720-039-3

12	22	100.0	5	17	US-10-497-628-15	Sequence 15, Appl
13	22	100.0	5	17	US-10-451-304-12	Sequence 12, Appl
14	22	100.0	5	19	US-11-018-690-4	Sequence 4, Appl
15	22	100.0	5	20	US-11-066-697-604	Sequence 604, App
16	22	100.0	5	20	US-11-025-494-3	Sequence 3, Appl
17	22	100.0	6	14	US-10-168-789A-38	Sequence 38, Appl
18	22	100.0	6	17	US-10-497-628-14	Sequence 14, Appl
19	22	100.0	6	20	US-11-066-697-5595	Sequence 595, App
20	22	100.0	6	20	US-11-066-697-5597	Sequence 597, App
21	22	100.0	6	20	US-11-066-697-601	Sequence 601, App
22	22	100.0	7	14	US-10-036-542-110	Sequence 110, App
23	22	100.0	7	14	US-10-036-542-111	Sequence 111, App
24	22	100.0	7	14	US-10-168-789A-37	Sequence 37, Appl
25	22	100.0	7	15	US-10-134-187-2	Sequence 2, Appl
26	22	100.0	7	15	US-10-688-741-2	Sequence 2, Appl
27	22	100.0	7	16	US-10-720-039-2	Sequence 13, Appl
28	22	100.0	7	17	US-10-497-628-13	Sequence 13, Appl
29	22	100.0	7	20	US-11-066-697-530	Sequence 530, App
30	22	100.0	7	20	US-11-066-697-556	Sequence 556, App
31	22	100.0	7	20	US-11-066-697-607	Sequence 607, App
32	22	100.0	7	20	US-11-025-494-2	Sequence 2, Appl
33	22	100.0	8	9	US-09-910-552-36	Sequence 36, Appl
34	22	100.0	8	14	US-10-168-789A-36	Sequence 36, Appl
35	22	100.0	8	15	US-10-643-465-36	Sequence 36, Appl
36	22	100.0	8	17	US-10-497-628-12	Sequence 12, Appl
37	22	100.0	8	20	US-11-066-697-5583	Sequence 583, App
38	22	100.0	8	20	US-11-066-697-5592	Sequence 592, App
39	22	100.0	8	20	US-11-066-697-600	Sequence 600, App
40	22	100.0	9	14	US-10-036-542-112	Sequence 112, App
41	22	100.0	9	14	US-10-168-789A-35	Sequence 35, App
42	22	100.0	9	15	US-10-134-187-1	Sequence 1, Appl
43	22	100.0	9	15	US-10-688-741-1	Sequence 1, Appl
44	22	100.0	9	16	US-10-720-039-1	Sequence 1, Appl
45	22	100.0	9	20	US-11-066-697-545	Sequence 545, App
46	22	100.0	9	20	US-11-066-697-622	Sequence 622, App
47	22	100.0	9	20	US-11-025-494-1	Sequence 1, Appl
48	22	100.0	10	9	US-09-853-161-110	Sequence 110, App
49	22	100.0	10	9	US-09-852-659A-110	Sequence 110, App
50	22	100.0	10	9	US-09-852-659A-110	Sequence 110, App
51	22	100.0	10	10	US-09-988-792-11	Sequence 11, Appl
52	22	100.0	10	10	US-10-197-954-98	Sequence 98, Appl
53	22	100.0	10	14	US-10-197-954-99	Sequence 99, Appl
54	22	100.0	10	14	US-10-168-789A-34	Sequence 34, Appl
55	22	100.0	10	14	US-10-267-918-1	Sequence 1, Appl
56	22	100.0	10	14	US-10-267-918-2	Sequence 2, Appl
57	22	100.0	10	15	US-10-058-993-110	Sequence 110, App
58	22	100.0	10	15	US-10-360-101-91	Sequence 91, Appl
59	22	100.0	10	15	US-10-445-400-1	Sequence 1, Appl
60	22	100.0	10	15	US-10-445-400-2	Sequence 2, Appl
61	22	100.0	10	17	US-10-718-071-6	Sequence 6, Appl
62	22	100.0	10	17	US-10-760-085-98	Sequence 98, Appl
63	22	100.0	10	17	US-10-760-085-99	Sequence 99, Appl
64	22	100.0	10	17	US-10-451-304-1	Sequence 1, Appl
65	22	100.0	10	17	US-10-451-304-2	Sequence 2, Appl
66	22	100.0	10	17	US-10-451-304-3	Sequence 3, Appl
67	22	100.0	10	18	US-10-994-170-1	Sequence 1, Appl
68	22	100.0	10	18	US-10-994-170-2	Sequence 2, Appl
69	22	100.0	10	18	US-10-951-993-110	Sequence 110, App
70	22	100.0	10	20	US-11-066-697-531	Sequence 531, App
71	22	100.0	10	20	US-11-066-697-532	Sequence 532, App
72	22	100.0	10	20	US-11-066-697-544	Sequence 544, App
73	22	100.0	10	20	US-11-066-697-546	Sequence 546, App
74	22	100.0	10	20	US-11-066-697-559	Sequence 559, App
75	22	100.0	10	20	US-11-066-697-573	Sequence 573, App
76	22	100.0	10	20	US-11-066-697-574	Sequence 574, App
77	22	100.0	10	20	US-11-066-697-621	Sequence 621, App
78	22	100.0	10	20	US-11-079-147-71	Sequence 71, Appl
79	22	100.0	11	9	US-09-265-690C-3	Sequence 3, Appl
80	22	100.0	11	9	US-09-935-682-64	Sequence 64, Appl
81	22	100.0	11	9	US-09-841-091B-26	Sequence 26, Appl
82	22	100.0	11	10	US-09-988-792-1	Sequence 1, Appl
83	22	100.0	11	10	US-09-988-792-6	Sequence 6, Appl
84	22	100.0	11	10	US-09-988-792-7	Sequence 7, Appl

85	22	100.0	11	10	US-09-988-792-8	Sequence 8, Appli
86	22	100.0	11	10	US-09-988-792-9	Sequence 9, Appli
87	22	100.0	11	10	US-09-988-792-10	Sequence 10, Appli
88	22	100.0	11	13	US-10-002-593-4	Sequence 4, Appli
89	22	100.0	11	14	US-10-230-133-1	Sequence 3, Appli
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; Publication No. US20010051345A1
; GENERAL INFORMATION:
; APPLICANT: Wellb, Ibert
; TITLE OF INVENTION: Method for Detecting Deficient Cellular Membrane Tightly Bound Mac
; FILE REFERENCE: 1427001
; CURRENT APPLICATION NUMBER: US/09/265,690C
; CURRENT FILING DATE: 1999-03-10
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: MOD RES
; LOCATION: (5)..(5)
; OTHER INFORMATION: AMIDATION
US-09-265-690C-1

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Best Local Similarity 80.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Db      1 FXGLM 5

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; Sequence 4, Application US/09265690C
; Publication No. US20010051345A1
; GENERAL INFORMATION:
; APPLICANT: Wellb, Ibert
; TITLE OF INVENTION: Method for Detecting Deficient Cellular Membrane Tightly Bound Mac
; FILE REFERENCE: 1427001
; CURRENT APPLICATION NUMBER: US/09/265,690C
; CURRENT FILING DATE: 1999-03-10
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: MOD RES
; LOCATION: (5)..(5)
; OTHER INFORMATION: AMIDATION
; NAME/KEY: VARIANT
; LOCATION: (2)..(2)
; OTHER INFORMATION: "X" may be either Phe or Val.
US-09-265-690C-4

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Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 FXGLM 5
Db      1 FXGLM 5

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; Sequence 4, Application US/10230133
; Publication No. US20030040625A1
; GENERAL INFORMATION:
; APPLICANT: Wellb, Ibert
; TITLE OF INVENTION: Antagonists of the magnesium binding defect as therapy agents and
; methods for treatment of abnormal physiological states

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OM protein - protein search, using sw model

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Perfect score: 22

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Minimum DB seq length: 0

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Pred. No. is the number of results predicted by chance to have a  
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and is derived by analysis of the total score distribution.

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7	22	100.0	5	1	US-08-391-814-1
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149	22 100.0	11 4 US-09-428-692-21
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 ; APPLICANT: Vaudry, Hubert  
 ; APPLICANT: Conlon, Michael J.  
 ; TITLE OF INVENTION: Neuropeptides of the Tachykinin Family  
 ; NUMBER OF SEQUENCES: 3  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Zarley, McKee, Thomte, Voornhees, and Sease  
 ; STREET: 801 Grand, Suite 3200  
 ; CITY: Des Moines  
 ; STATE: Iowa  
 ; COUNTRY: United States  
 ; ZIP: 50309  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patentin Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/07/753, 909B  
 ; FILING DATE: 19910903  
 ; CLASSIFICATION: 530  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: FR 9106759  
 ; FILING DATE: 04-JUN-1991  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Sease, Edmund J.  
 ; REGISTRATION NUMBER: 24,741  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (515)-288-3667  
 ; TELEFAX: (515)-288-1338  
 ; INFORMATION FOR SEQ ID NO: 3:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 5 amino acids  
 ; TYPE: AMINO ACID  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: peptide  
 ; FRAGMENT TYPE: C-terminal  
 ; ORIGINAL SOURCE:  
 ; ORGANISM: Rana ridibunda  
 ; DEVELOPMENTAL STAGE: adult  
 ; TISSUE TYPE: brain  
 ; US-07-753-909B-3

Query Match 100.0%; Score 22; DB 1; Length 5;  
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 ; Sequence 2, Application US/07934553  
 ; Patent No. 5314690  
 ; GENERAL INFORMATION:  
 ; APPLICANT: PATTERSON, ROY  
 ; APPLICANT: HARRIS, KATHLEEN E  
 ; TITLE OF INVENTION: METHOD AND COMPOSITION FOR REDUCING IGE  
 ; NUMBER OF SEQUENCES: 5  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: TILTON, FALLON, LUNGKUS & CHESTNUT  
 ; STREET: 100 SOUTH WACKER DRIVE  
 ; CITY: CHICAGO  
 ; STATE: ILLINOIS  
 ; COUNTRY: USA  
 ; ZIP: 60606-4002  
 ; COMPUTER READABLE FORM:  
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 ; OPERATING SYSTEM: IBM PC compatible  
 ; SOFTWARE: Patentin Release #1.0, Version #1.25  
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 ; FILING DATE: 19920821  
 ; CLASSIFICATION: 424  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 07/705, 071  
 ; FILING DATE: 24-MAY-1991  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: FENTRESS, SUSAN B  
 ; REGISTRATION NUMBER: 31,327  
 ; REFERENCE/DOCKET NUMBER: NU-9033CIP  
 ; TELECOMMUNICATION INFORMATION:



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Title: US-10-053-669-4

Perfect score: 22

Sequence: 1 FXGLM 5

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2105692

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Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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2: geneseqp19908:.\*  
3: geneseqp20008:.\*  
4: geneseqp20018:.\*  
5: geneseqp20028:.\*  
6: geneseqp20038:.\*  
7: geneseqp20048:.\*  
8: geneseqp20058:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Match length	ID	Description
1	22	100.0	5 2 AAR33009	Aar33009 Alpha-sub
2	22	100.0	5 2 AAR33008	Aar33008 Alpha-sub
3	22	100.0	5 2 AAR33007	Aar33007 Alpha-sub
4	22	100.0	5 2 AAR33010	Aar33010 Alpha-sub
5	22	100.0	5 2 AAR60134	Aar60134 COOH-term
6	22	100.0	5 2 AAR54549	Aar54549 Cholecyt
7	22	100.0	5 2 AAR54551	Aar54551 Cholecyt
8	22	100.0	5 2 AAR54550	Aar54550 Cholecyt
9	22	100.0	5 2 AAR54548	Aar54548 Cholecyt
10	22	100.0	5 2 AAR41687	Aar41687 Tetrapt
11	22	100.0	5 2 AAR96643	Aar96643 Substance
12	22	100.0	5 2 AAY50325	Aay50325 Neutroph
13	22	100.0	5 2 AAW92660	Aaw92660 Human tac
14	22	100.0	5 3 AAB23028	Aab23028 Mammalian
15	22	100.0	5 3 AAB23025	Aab23025 Human/rat
16	22	100.0	5 3 AAT67576	Aat67576 P antgon
17	22	100.0	5 4 AAB66674	Aab66674 C-term
18	22	100.0	5 4 AAB82430	Aab82430 Fluorinat
19	22	100.0	5 4 AAB82431	Aab82431 Fluorinat
20	22	100.0	5 4 AAB91428	Aab91428 Tachykin
21	22	100.0	5 4 AAB70556	Aab70556 Octopus t
22	22	100.0	5 5 AAB10088	Aab10088 Human bet
23	22	100.0	5 5 AAB10088	Aab10088 Substance
24	22	100.0	5 5 AAU77847	Aau77847 Tachykin
25	22	100.0	5 5 AAU77845	Aau77845 Tachykin

26	22	100.0	5 7 ADC64000	Adc64000 Tachykin
27	22	100.0	5 7 ADE94203	Ade94203 High acti
28	22	100.0	5 7 ADF92530	Adf92530 Substance
29	22	100.0	5 8 ADN12180	Adn12180 Tachykin
30	22	100.0	5 8 ADN95078	Adn95078 Mammalian
31	22	100.0	5 8 ADR43774	Adr43774 Mammalian
32	22	100.0	5 8 ADR43771	Adr43771 Human mag
33	22	100.0	6 1 AAP30443	Aap30443 Sequence
34	22	100.0	6 1 AAP40519	Aap40519 Sequence
35	22	100.0	6 1 AAP50694	Aap50694 Sequence
36	22	100.0	6 1 AAP50632	Aap50632 Substance
37	22	100.0	6 1 AAP61486	Aap61486 Peptide h
38	22	100.0	6 2 AAR07897	Aar07897 Cyclopept
39	22	100.0	6 2 AAR07893	Aar07893 Cyclopept
40	22	100.0	6 2 AAR21959	Aar21959 Substance
41	22	100.0	6 2 AAR27696	Aar27696 Cyclic ta
42	22	100.0	6 2 AAR27694	Aar27694 Cyclic ta
43	22	100.0	6 2 AAR27695	Aar27695 Cyclic ta
44	22	100.0	6 2 AAW9686	Aaw9686 Substance
45	22	100.0	6 2 AAW92706	Aaw92706 Human tac
46	22	100.0	6 2 AAW92659	Aaw92659 Human tac
47	22	100.0	6 2 AAY1052	Aay1052 Non-cross
48	22	100.0	6 3 AAT67575	Aat67575 P antgon
49	22	100.0	6 4 AAB82453	Aab82453 Fluorinat
50	22	100.0	6 4 AAB82432	Aab82432 Fluorinat
51	22	100.0	6 4 AAB82436	Aab82436 Fluorinat
52	22	100.0	6 4 AAB82433	Aab82433 Fluorinat
53	22	100.0	6 4 AAB81421	Aab81421 Tachykin
54	22	100.0	6 4 AAB81425	Aab81425 Tachykin
55	22	100.0	6 4 AAB81419	Aab81419 Tachykin
56	22	100.0	6 4 AAG99351	Aag99351 Aclypical
57	22	100.0	6 4 AAB74306	Aab74306 Peptide a
58	22	100.0	6 4 AAB98884	Aab98884 Chimeric
59	22	100.0	6 4 AAB98886	Aab98886 Chimeric
60	22	100.0	6 5 AAB10087	Aab10087 Substance
61	22	100.0	6 5 AAB10086	Aab10086 Substance
62	22	100.0	6 6 AAB137288	Abj37288 Rhodopsin
63	22	100.0	7 ADE94202	Ade94202 High acti
64	22	100.0	7 1 AAP20310	Aap20310 TyR8-SP5-
65	22	100.0	7 2 AAR21956	Aar21956 Substance
66	22	100.0	7 2 AAR21957	Aar21957 Substance
67	22	100.0	7 2 AAW92539	Aaw92539 Asp-Ser-P
68	22	100.0	7 2 AAY50324	Aay50324 Neutroph
69	22	100.0	7 2 AAW92662	Aaw92662 Human tac
70	22	100.0	7 2 AAW92705	Aaw92705 Human tac
71	22	100.0	7 3 AAT67574	Aat67574 P antgon
72	22	100.0	7 4 AAB80323	Aab80323 Human pro
73	22	100.0	7 4 AAB80324	Aab80324 Human pro
74	22	100.0	7 4 AAB82428	Aab82428 Fluorinat
75	22	100.0	7 4 AAB82429	Aab82429 Fluorinat
76	22	100.0	7 4 AAB81354	Aab81354 Tachykin
77	22	100.0	7 4 AAB81431	Aab81431 Tachykin
78	22	100.0	7 4 AAB81420	Aab81420 Tachykin
79	22	100.0	7 4 AAG99350	Aag99350 Aclypical
80	22	100.0	7 4 AAB98845	Aab98845 Chimeric
81	22	100.0	7 5 AAB10085	Aab10085 Substance
82	22	100.0	7 5 ABB09500	Abb09500 Substance
83	22	100.0	7 7 ADE94201	Ade94201 High acti
84	22	100.0	7 7 ADF92529	Adf92529 Substance
85	22	100.0	7 8 ADN95077	Adn95077 Mammalian
86	22	100.0	8 1 AAP20303	Aap20303 Gastroint
87	22	100.0	8 2 AAR28444	Aar28444 Neurokin
88	22	100.0	8 2 AAW57536	Aaw57536 Molecular
89	22	100.0	8 2 AAW92664	Aaw92664 Human tac
90	22	100.0	8 2 AAW92710	Aaw92710 Human tac
91	22	100.0	8 3 AAY67573	Aay67573 P antgon
92	22	100.0	8 4 AAB91407	Aab91407 Tachykin
93	22	100.0	8 4 AAB91416	Aab91416 Tachykin
94	22	100.0	8 4 AAB91424	Aab91424 Tachykin
95	22	100.0	8 4 AAG99349	Aag99349 Aclypical
96	22	100.0	8 4 AAB97571	Aab97571 Substictut
97	22	100.0	8 5 AAB09498	Abb09498 Substance
98	22	100.0	8 5 AAB09499	Abb09499 Substance

99	22	100.0	8	7	ADB94200	Ad994200 High acti
100	22	100.0	9	1	AAp50634	AAp50634 Substance
101	22	100.0	9	2	AAW92714	AAW92714 Human tac
102	22	100.0	9	4	AAAB80325	AAAB80325 Human pro
103	22	100.0	9	4	AAAB91446	AAAB91446 Tachykini
104	22	100.0	9	4	AAAB91369	AAAB91369 Tachykini
105	22	100.0	9	4	AAAG99348	AAAG99348 Tachykini
106	22	100.0	9	7	ADf92528	ADf92528 Substance
107	22	100.0	9	8	ADN95076	ADN95076 Mammalian
108	22	100.0	10	1	AAp40414	AAp40414 Decapepti
109	22	100.0	10	1	AAp40413	AAp40413 Substance
110	22	100.0	10	1	AAp50633	AAp50633 Substance
111	22	100.0	10	2	AAAR21933	AAAR21933 Substance
112	22	100.0	10	2	AAAR5181	AAAR5181 S. cerevi
113	22	100.0	10	2	AAAR77311	AAAR77311 Neurokint
114	22	100.0	10	2	AAAR77312	AAAR77312 Neurokint
115	22	100.0	10	2	AAAW79777	AAAW79777 Neurokint
116	22	100.0	10	2	AAAW9776	AAAW9776 Neurokint
117	22	100.0	10	2	AAAM8951	AAAM8951 Tachykini
118	22	100.0	10	2	AAAM75251	AAAM75251 Fragment
119	22	100.0	10	2	AAW74415	AAW74415 HPMBO91 p
120	22	100.0	10	2	AAAY3264	AAAY3264 Protein b
121	22	100.0	10	2	AAAY06939	AAAY06939 Substance
122	22	100.0	10	2	AAW92663	AAW92663 Human tac
123	22	100.0	10	2	AAW92697	AAW92697 Human tac
124	22	100.0	10	2	AAW92698	AAW92698 Human tac
125	22	100.0	10	2	AAW92729	AAW92729 Human tac
126	22	100.0	10	2	AAW92696	AAW92696 Human tac
127	22	100.0	10	2	AAW92728	AAW92728 Human tac
128	22	100.0	10	4	AAAB82417	AAAB82417 Neurokint
129	22	100.0	10	4	AAAB81383	AAAB81383 Tachykini
130	22	100.0	10	4	AAAB91398	AAAB91398 Tachykini
131	22	100.0	10	4	AAAB91355	AAAB91355 Tachykini
132	22	100.0	10	4	AAAB91397	AAAB91397 Tachykini
133	22	100.0	10	4	AAAB91370	AAAB91370 Tachykini
134	22	100.0	10	4	AAAB91368	AAAB91368 Tachykini
135	22	100.0	10	4	AAAB81445	AAAB81445 Tachykini
136	22	100.0	10	4	AAAB91356	AAAB91356 Tachykini
137	22	100.0	10	4	AAAG99355	AAAG99355 Neurokint
138	22	100.0	10	4	AAAG99356	AAAG99356 Neurokint
139	22	100.0	10	4	AAAG99347	AAAG99347 ATypical
140	22	100.0	10	4	AAAG64746	AAAG64746 Substance
141	22	100.0	10	4	AAAB82381	AAAB82381 Human neu
142	22	100.0	10	5	AAAE27017	AAAE27017 Human gen
143	22	100.0	10	5	AAAE27155	AAAE27155 Human gen
144	22	100.0	10	5	AAAB99004	AAAB99004 Neurokint
145	22	100.0	10	6	AAAB99003	AAAB99003 Neurokint
146	22	100.0	10	6	AAAG76074	AAAG76074 Sea lamp
147	22	100.0	10	6	ABU65028	ABU65028 Human sec
148	22	100.0	10	7	ADCG3999	ADCG3999 Mosquito
149	22	100.0	10	7	ADCG3998	ADCG3998 Mosquito
150	22	100.0	10	8	ADG89837	ADG89837 Human sec

## ALIGNMENTS

RESULT 1  
 AAR33009  
 ID AAR33009 standard; peptide; 5 AA.  
 XX  
 AC AAR33009;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 02-APR-1993 (first entry)  
 XX  
 XX Alpha-substituted short peptide.  
 DE  
 XX CCK; neuropeptide; endorphin; hormone; LHRH; contrareception; analgesia;  
 KW improved bioavailability.  
 XX  
 OS Synthetic.  
 XX

PH	Key	Location/Qualifiers
FT	Modified-site	4 /note= "alpha-Me-Leu"
FT	Modified-site	5 /note= "Met-NH2"
PN	MO9219254-A1.	
XX	12-NOV-1992.	
PD	15-APR-1992; 92WC-US003119.	
PF	24-APR-1991; 91US-00690755.	
PR	20-MAR-1992; 92US-00852086.	
XX	(WARN ) WARNER LAMBERT CO.	
PA	Horwell DC, Hughes J, Richardson RS, Howson W;	
PI	WPI, 1992-398522/48.	
XX	New alpha-subst. polypeptide are e.g. selective receptor ligands - for	
PT	treating inflammation, pain, stroke, ulcers, hypertension, heart failure,	
PT	depression, cancer, asthma, psychosis, arthritis, etc.	
XX	Claim 3; Page 41; 46pp; English.	
PS	The peptide is a specifically claimed example of a group of generically	
XX	claimed mono-, di-, tri-, tetra- and penta-peptides which include a	
CC	substituent on an alpha-C atom in the chain. Such substitution may modify	
CC	the bioavailability, stability or absorbability of the peptide and hence	
CC	may improve the activity of the peptide as a drug. Depending on the	
CC	nature of the parent peptide (hormone, endorphin, CCK, NK2, chemotactic	
CC	peptide, etc.), the modified peptides are variously useful for treating	
CC	obesity, anxiety, gastrointestinal ulcers, pain, stroke, inflammation,	
CC	addictive drug withdrawal symptoms, hypertension, heart failure,	
CC	cognition or memory disorders, spasticity, depression, diabetes, cancer,	
CC	asthma, bladder dysfunction, psychosis and arthritis; and as	
CC	contraceptives. (Updated on 25-MAR-2003 to correct PN field.) (Updated on	
CC	25-MAR-2003 to correct PD field.) (Updated on 25-MAR-2003 to correct PR	
CC	field.) (Updated on 25-MAR-2003 to correct PI field.)	
XX		
SO	Sequence 5 AA;	
QY	Query Match	100.0%; Score 22; DB 2; Length 5;
Db	Best Local Similarity	80.0%; Pred. No. 1.8e+06;
	Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	
	1 FXGLM 5	
	1 FXGLM 5	
RESULT 2		
AAR33008		
ID AAR33008 standard; peptide; 5 AA.		
XX		
AC AAR33008;		
XX		
DT 25-MAR-2003 (revised)		
DT 02-APR-1993 (first entry)		
XX		
XX Alpha-substituted short peptide.		
DE		
XX CCK; neuropeptide; endorphin; hormone; LHRH; contrareception; analgesia;		
KW improved bioavailability.		
XX		
OS Synthetic.		
XX		
FT Key	Location/Qualifiers	
FT Modified-site	2 /note= "alpha-Me-Phe"	
FT Modified-site	5 /note= "alpha-Me-Phe"	

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 26, 2005, 08:25:34 ; Search time 169 Seconds

(without alignments)  
15.150 Million cell updates/sec

Title: US-10-053-669-4  
Perfect score: 22  
Sequence: 1 FXGLM 5

Scoring table: BIOSUM62DX  
Gapop.10.0 ; Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 3223

Minimum DB seq length: 0  
Maximum DB seq length: 11

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 150 summaries

Database: Uniprot\_03.\*  
1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	22	100.0	10	1	TKN1_SCYCA
2	22	100.0	10	1	TKNB_CHICK
3	22	100.0	10	1	TKNB_ONCMY
4	22	100.0	10	1	TKNB_RANCA
5	22	100.0	10	1	TKNB_RANRI
6	22	100.0	10	1	TKNC_RANCA
7	22	100.0	10	1	TKNK_PIG
8	22	100.0	10	1	TKNK_RANRI
9	22	100.0	10	1	TKNK_RANRI
10	22	100.0	10	1	TKN1_EHARI
11	22	100.0	10	1	TKS1_AEDAE
12	22	100.0	10	1	TKS2_AEDAE
13	22	100.0	10	1	TKN1_PSEGU
14	22	100.0	10	1	TKN1_PSEGU
15	22	100.0	10	1	TKN1_PSEGU
16	22	100.0	10	1	TKN2_PSEGU
17	22	100.0	10	1	TKN2_PSEGU
18	22	100.0	10	1	TKN3_PSEGU
19	22	100.0	10	1	TKN4_PSEGU
20	22	100.0	10	1	TKN5_PSEGU
21	22	100.0	10	1	TKNA_CAYPO
22	22	100.0	10	1	TKNA_CAYPO
23	22	100.0	10	1	TKNA_CHICK
24	22	100.0	10	1	TKNA_GAMMO
25	22	100.0	10	1	TKNA_HORSE
26	22	100.0	10	1	TKNA_RANCA
27	22	100.0	10	1	TKNA_RANCA
28	22	100.0	10	1	TKNA_RANRI
29	22	100.0	10	1	TKNA_SCYCA
30	22	100.0	10	1	TKN_ELECT
31	22	100.0	10	1	TKN_PHYFU
32	22	100.0	10	2	Q9UAR8

32	17	77.3	10	2	Q6J9J7	Q6J9J7 neisseria g
33	16	72.7	10	2	Q35013	Q35013 meloidogyne
34	16	72.7	10	2	Q76ML8	Q76ML8 eurypharynx
35	16	72.7	10	2	Q7M278	Q7M278 cricium tu
36	15	68.2	9	1	TRP4_LEUMA	TRP4_LEUMA
37	15	68.2	9	2	Q7M3L3	Q7M3L3 penaeus van
38	15	68.2	10	1	TRP6_LEUMA	TRP6_LEUMA
39	15	68.2	10	1	TRP7_LEUMA	TRP7_LEUMA
40	15	68.2	10	1	TRP8_LEUMA	TRP8_LEUMA
41	15	68.2	10	1	TRP9_LEUMA	TRP9_LEUMA
42	15	68.2	11	2	Q9R446	Q9R446 neisseria g
43	14	63.6	9	1	TKC1_CALVO	TKC1_CALVO
44	14	63.6	9	2	TKL1_LOOMI	TKL1_LOOMI
45	14	63.6	10	2	Q85599	Q85599 moloney mur
46	14	63.6	10	1	TKL2_LOOMI	TKL2_LOOMI
47	14	63.6	10	1	TKL3_LOOMI	TKL3_LOOMI
48	14	63.6	10	1	TKL4_LOOMI	TKL4_LOOMI
49	14	63.6	10	1	TRP5_LEUMA	TRP5_LEUMA
50	14	63.6	11	1	TKC2_CALVO	TKC2_CALVO
51	13	59.1	5	1	TPIS_CANFA	TPIS_CANFA
52	13	59.1	7	1	PPH2_LYCES	PPH2_LYCES
53	13	59.1	8	1	CCRN_DASVI	CCRN_DASVI
54	13	59.1	8	1	CCRN_MACEU	CCRN_MACEU
55	13	59.1	8	1	TXV1_PICNI	TXV1_PICNI
56	13	59.1	8	2	Q94VF3	Q94VF3
57	13	59.1	8	2	Q09258	Q09258
58	13	59.1	9	1	CAER_PHYSA	CAER_PHYSA
59	13	59.1	9	1	CCAP_SPOER	CCAP_SPOER
60	13	59.1	9	1	CCAP_TENMO	CCAP_TENMO
61	13	59.1	9	1	FIBB_ERYPA	FIBB_ERYPA
62	13	59.1	9	1	FIBB_MACFU	FIBB_MACFU
63	13	59.1	9	1	FIBB_PAPAN	FIBB_PAPAN
64	13	59.1	9	1	FIBB_PAPAN	FIBB_PAPAN
65	13	59.1	9	1	FIBB_THEGE	FIBB_THEGE
66	13	59.1	9	1	RE42_LITRU	RE42_LITRU
67	13	59.1	9	1	SAMP_MUSCA	SAMP_MUSCA
68	13	59.1	9	2	Q7M3N6	Q7M3N6
69	13	59.1	9	2	Q8M3N1	Q8M3N1
70	13	59.1	9	2	Q8M3N2	Q8M3N2
71	13	59.1	9	2	Q8M3N3	Q8M3N3
72	13	59.1	9	2	Q8M3N4	Q8M3N4
73	13	59.1	9	2	Q8M3N5	Q8M3N5
74	13	59.1	9	2	Q8M3N6	Q8M3N6
75	13	59.1	9	2	Q8M3N7	Q8M3N7
76	13	59.1	9	2	Q8M3N8	Q8M3N8
77	13	59.1	9	2	Q8M3N9	Q8M3N9
78	13	59.1	9	2	Q7M2M7	Q7M2M7
79	13	59.1	9	2	Q67AR4	Q67AR4
80	13	59.1	9	2	Q67AR6	Q67AR6
81	13	59.1	9	2	Q67AR7	Q67AR7
82	13	59.1	9	2	Q67AT1	Q67AT1
83	13	59.1	9	2	Q67AT2	Q67AT2
84	13	59.1	9	2	Q30790	Q30790
85	13	59.1	10	1	CAER_LITXA	CAER_LITXA
86	13	59.1	10	1	DYSE_LITXA	DYSE_LITXA
87	13	59.1	10	1	PRCK_FASHE	PRCK_FASHE
88	13	59.1	10	1	TKU1_UREUN	TKU1_UREUN
89	13	59.1	10	1	TKU2_UREUN	TKU2_UREUN
90	13	59.1	10	1	TPIS_NICPL	TPIS_NICPL
91	13	59.1	10	2	Q7M4X1	Q7M4X1
92	13	59.1	10	2	Q7M4X7	Q7M4X7
93	13	59.1	10	2	Q7M4X2	Q7M4X2
94	13	59.1	10	2	Q25355	Q25355
95	13	59.1	10	2	Q25356	Q25356
96	13	59.1	10	2	Q25357	Q25357
97	13	59.1	10	2	Q6P2D4	Q6P2D4
98	13	59.1	10	2	Q6P2D4	Q6P2D4
99	13	59.1	10	2	Q6U014	Q6U014
100	13	59.1	10	2	Q6U015	Q6U015
101	13	59.1	10	2	Q64ET6	Q64ET6
102	13	59.1	10	2	Q6EX62	Q6EX62
103	13	59.1	10	2	Q71VN2	Q71VN2
104	13	59.1	10	2	Q71ZC5	Q71ZC5

105	13	59.1	11	1	RE41_LITRU	P82074	litorea rub
106	13	59.1	11	2	Q9UC46	Q9UC46	homo sapien
107	13	59.1	11	2	Q9TWM2	Q9TWM2	apiysia cal
108	13	59.1	11	2	Q9S319	Q9S319	eulemur ful
109	13	59.1	11	2	Q9S320	Q9S320	eulemur ful
110	13	59.1	11	2	Q9S320	Q9S320	eulemur ful
111	13	59.1	11	2	Q9S320	Q9S320	eulemur ful
112	13	59.1	11	2	Q9S320	Q9S320	eulemur ful
113	13	59.1	11	2	Q9S320	Q9S320	eulemur ful
114	13	59.1	11	2	Q9S320	Q9S320	eulemur ful
115	13	59.1	11	2	Q9S320	Q9S320	eulemur ful
116	13	59.1	11	2	Q9S320	Q9S320	eulemur ful
117	13	59.1	11	2	Q9S320	Q9S320	eulemur ful
118	13	59.1	11	2	Q9S320	Q9S320	eulemur ful
119	13	59.1	11	2	Q9S320	Q9S320	eulemur ful
120	13	59.1	11	2	Q9S320	Q9S320	eulemur ful
121	13	59.1	11	2	Q9S320	Q9S320	eulemur ful
122	13	59.1	11	2	Q9S320	Q9S320	eulemur ful
123	13	59.1	11	2	Q9S320	Q9S320	eulemur ful
124	13	59.1	11	2	Q9S320	Q9S320	eulemur ful
125	13	59.1	11	2	Q9S320	Q9S320	eulemur ful
126	13	59.1	11	2	Q9S320	Q9S320	eulemur ful
127	13	59.1	11	2	Q9S320	Q9S320	eulemur ful
128	13	59.1	11	2	Q9S320	Q9S320	eulemur ful
129	13	59.1	11	2	Q9S320	Q9S320	eulemur ful
130	13	59.1	11	2	Q9S320	Q9S320	eulemur ful
131	13	59.1	11	2	Q9S320	Q9S320	eulemur ful
132	13	59.1	11	2	Q9S320	Q9S320	eulemur ful
133	13	59.1	11	2	Q9S320	Q9S320	eulemur ful
134	13	59.1	11	2	Q9S320	Q9S320	eulemur ful
135	13	59.1	11	2	Q9S320	Q9S320	eulemur ful
136	13	59.1	11	2	Q9S320	Q9S320	eulemur ful
137	13	59.1	11	2	Q9S320	Q9S320	eulemur ful
138	13	59.1	11	2	Q9S320	Q9S320	eulemur ful
139	13	59.1	11	2	Q9S320	Q9S320	eulemur ful
140	13	59.1	11	2	Q9S320	Q9S320	eulemur ful
141	13	59.1	11	2	Q9S320	Q9S320	eulemur ful
142	13	59.1	11	2	Q9S320	Q9S320	eulemur ful
143	13	59.1	11	2	Q9S320	Q9S320	eulemur ful
144	13	59.1	11	2	Q9S320	Q9S320	eulemur ful
145	13	59.1	11	2	Q9S320	Q9S320	eulemur ful
146	13	59.1	11	2	Q9S320	Q9S320	eulemur ful
147	13	59.1	11	2	Q9S320	Q9S320	eulemur ful
148	13	59.1	11	2	Q9S320	Q9S320	eulemur ful
149	13	59.1	11	2	Q9S320	Q9S320	eulemur ful
150	13	59.1	11	2	Q9S320	Q9S320	eulemur ful

## ALIGNMENTS

RESULT 1  
TKNB\_SCVCA STANDARD; PRT; 10 AA.  
AC P08608;  
DT 01-AUG-1988 (Rel. 08, Created)  
DT 01-AUG-1988 (Rel. 08, Last sequence update)  
DT 05-JUN-2004 (Rel. 44, Last annotation update)  
DE Scyllorhinus I.  
OS Scyllorhinus canicula (Spotted dogfish) (Spotted catshark).  
OC Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;  
OC Elasmobranchii; Galeomorphi; Galeoidea; Carcharhiniformes;  
OC Scyllorhinidae; Scyllorhinus.  
NCBI\_TaxID=7830;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Intestine; PubMed=2422058; DOI=10.1016/0014-5793(86)80521-X;  
RA Conlon J.M., Deacon C.F., O'Toole L., Thim L.;  
RT "Scyllorhinus I and II: two novel tachykinins from dogfish gut."  
RL FEBS Lett. 200:111-116(1986).  
RN [2]  
RP SEQUENCE.

RC TISSUE=Brain; PubMed=7685693;  
RX MEDLINE=93292508; Balmert R.J., Conlon J.M.;  
RA Maugh D., Wang Y., Hazon N., Balmert R.J., Conlon J.M.;  
RT "Primary structures and biological activities of substance-P-related  
peptides from the brain of the dogfish, Scyllorhinus canicula."  
Eur. J. Biochem. 214:469-474(1993).  
RU [1]  
CC -1- FUNCTION: Tachykinins are active peptides which excite neurons,  
evoked behavioral responses, are potent vasodilators and  
secretagogues, and contract (directly or indirectly) many smooth  
muscles.  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- SIMILARITY: Belongs to the tachykinin family.  
DR PIR; A24867; A24867.  
DR InterPro; IPR002040; Tachy Neurokinin.  
DR PROSITE; PS00267; TACHYKININ, 1.  
KM Amidation; Direct protein sequencing; Neuropeptide; Tachykinin.  
FT MOD RES 10 10 Methionine amide.  
SQ SEQUENCE 10 AA; 1219 MW; D0602D6B59C33AA9 CRC64;

Query Match 100.0%; Score 22; DB 1; Length 10;  
Best Local Similarity 80.0%; Pred. No. 1.4e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXGLM 5  
DB 6 FXGLM 10

RESULT 2  
TKNB\_CHICK STANDARD; PRT; 10 AA.  
AC P19851;  
DT 01-FEB-1991 (Rel. 17, Created)  
DT 01-FEB-1991 (Rel. 17, Last sequence update)  
DT 25-OCT-2004 (Rel. 45, Last annotation update)  
DE Neurokinin A (Substance K) (Neuromedin L).  
OS Gallus gallus (Chicken).  
OC Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
OC Gallus.  
NCBI\_TaxID=9031;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Intestine; PubMed=2452461; DOI=10.1016/0167-0115(88)90050-X;  
RX MEDLINE=88204263; Conlon J.M., Katsoulis S., Schmidt W.E., Thim L.;  
RA "Arg3]ubstance P and neurokinin A from chicken small intestine."  
Regul. Pept. 20:171-180(1988).  
RT -1- FUNCTION: Tachykinins are active peptides which excite neurons,  
evoked behavioral responses, are potent vasodilators and  
secretagogues, and contract (directly or indirectly) many smooth  
muscles.  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- SIMILARITY: Belongs to the tachykinin family.  
DR PIR; UN0024; UN0024.  
DR PDB; 1N6T; NMR; A=1-10.  
DR InterPro; IPR002040; Tachy Neurokinin.  
DR Pfam; PF02202; Tachykinin, 1.  
DR PROSITE; PS00267; TACHYKININ, 1.  
KM 3D-structure; Amidation; Direct protein sequencing; Neuropeptide;  
KW Tachykinin.  
FT MOD RES 10 10 Methionine amide.  
SQ SEQUENCE 10 AA; 1134 MW; 8A6B4062C9D5BABA1 CRC64;

Query Match 100.0%; Score 22; DB 1; Length 10;  
Best Local Similarity 80.0%; Pred. No. 1.4e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXGLM 5  
DB 6 FXGLM 10

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OM protein - protein search, using bw model

Run on: October 26, 2005, 08:26:18 ; Search time 37 Seconds  
(without alignments)  
13.002 Million cell updates/sec

Title: US-10-053-669-4  
Perfect score: 22  
Sequence: 1 FXGLM 5

Scoring table: BLASTSUM320X  
Gapop: 10.0, Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 1328

Minimum DB-seq length: 0  
Maximum DB-seq length: 11

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 150 summaries

Database: us-10-053-669-4  
1: p1r1:\*  
3: p1r2:\*  
4: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	22	100.0	10	1	SPPGK	neuromedin K - pig
2	22	100.0	10	2	JN0024	neurokinin A - chi
3	22	100.0	10	2	B49581	galactin II - ye
4	22	100.0	10	2	A49581	galactin I - ye
5	22	100.0	10	2	A24867	acylornitin I - s
6	22	100.0	10	2	S23307	neurokinin A - rat
7	22	100.0	10	2	S23386	neurokinin A - Act
8	22	100.0	10	2	S07202	phyllomedulin - tw
9	22	100.0	10	2	G61033	ranatichykinin C -
10	22	100.0	10	2	B61033	ranatichykinin B -
11	22	100.0	10	2	S27178	neurokinin A-relac
12	22	100.0	11	1	A60654	substance P - guin
13	22	100.0	11	1	EOCC	eledoisin - musky
14	22	100.0	11	1	EOCC	eledoisin - musky
15	22	100.0	11	1	SPHO	eledoisin - musky
16	22	100.0	11	2	JN0023	substance P - hors
17	22	100.0	11	2	S33300	substance P - chic
18	22	100.0	11	2	S07203	probable substance
19	22	100.0	11	2	G60409	uperclelele - frog
20	22	100.0	11	2	E60409	kassinin-like pept
21	22	100.0	11	2	E60409	substance P-like p
22	22	100.0	11	2	B60409	kassinin-like pept
23	22	100.0	11	2	D60409	substance P-like p
24	22	100.0	11	2	S23308	kassinin-like pept
25	22	100.0	11	2	S23306	substance P - rain
26	22	100.0	11	2	S07201	substance P - Acta
27	22	100.0	11	2	A61033	physalaemin - frog
28	22	100.0	11	2	PT0249	ranatichykinin A -
29	16	72.7	10	2	S19296	16k protein - pou

30	15	68.2	5	2	A61445	Met-enkephalin - b
31	15	68.2	7	2	A60224	Met-enkephalin-Arg
32	15	68.2	9	2	PT0225	Ig heavy chain CDR
33	15	68.2	9	2	PD0027	pev-rachykinin - p
34	14	63.6	4	2	PT0240	Ig heavy chain CRD
35	14	63.6	10	1	ECLQ1M	tachykinin I - mlg
36	14	63.6	10	1	ECLQ3M	tachykinin III - m
37	14	63.6	10	1	ECLQ4M	tachykinin IV - m
38	14	63.6	10	2	S68033	cytochrome P450 1A
39	14	63.6	11	1	ECLQ2M	tachykinin II - mi
40	13	59.1	5	2	PT0278	Ig heavy chain CRD
41	13	59.1	6	2	A61049	halo-toxin - Pseud
42	13	59.1	7	2	H33098	180K exoantigen -
43	13	59.1	7	2	E33932	Ig mu chain D regi
44	13	59.1	8	2	P00012	cholecystokinin -
45	13	59.1	8	2	A43001	cholecystokinin -
46	13	59.1	8	2	S13661	polygalacturonase
47	13	59.1	8	2	A42057	fibroblast growth
48	13	59.1	8	2	PC4372	telomeric and tetr
49	13	59.1	8	2	A46306	spasmogenic toxin
50	13	59.1	9	2	A61357	phyllotoxin beta ch
51	13	59.1	9	2	D24180	fibrirogen beta ch
52	13	59.1	9	2	C24180	fibrirogen beta ch
53	13	59.1	9	2	E28854	fibriropeptide B -
54	13	59.1	9	2	F28854	fibriropeptide B -
55	13	59.1	9	2	D28854	fibriropeptide B -
56	13	59.1	9	2	S39766	cardioactive pepti
57	13	59.1	9	2	PH0942	cardioactive pepti
58	13	59.1	9	2	S39767	cardioactive pepti
59	13	59.1	9	2	A26363	cardioactive pepti
60	13	59.1	9	2	D57444	neuropeptide Grb-A
61	13	59.1	9	2	S27233	cardioactive pepti
62	13	59.1	9	2	B20569	serum amyloid P-co
63	13	59.1	9	2	S10784	enamelin I - bovin
64	13	59.1	10	2	A61337	caerulein - frog
65	13	59.1	10	2	A13687	caerulein-like pep
66	13	59.1	10	2	H28027	protein p11 - curl
67	13	59.1	10	2	S71948	matrix metalloprot
68	13	59.1	10	2	C39398	Fe mu (IGM) recept
69	13	59.1	10	2	PH0807	T-cell receptor al
70	13	59.1	10	2	A27617	triose-phosphate 1
71	13	59.1	10	2	PN0165	triose-phosphate 1
72	13	59.1	10	2	A59173	nuclease Bhl (EC 3
73	13	59.1	11	2	A33917	dihydroorotase (EC
74	13	59.1	11	2	A35594	buccalin - Callifor
75	12	54.5	5	2	B61445	leu-enkephalin - b
76	12	54.5	9	2	D44787	callifmrinamide 13
77	12	54.5	10	2	A60410	beta-neoendorphin
78	12	54.5	10	2	PT0310	Ig heavy chain CRD
79	12	54.5	11	2	PT0301	Ig heavy chain CRD
80	11	50.0	5	2	G44817	27.5 kda structura
81	11	50.0	5	2	I44817	27.5 kda structura
82	11	50.0	5	2	E44817	27.5 kda structura
83	11	50.0	5	2	E44817	27.5 kda structura
84	11	50.0	5	2	A44817	28K structural pro
85	11	50.0	6	2	PT0643	T-cell receptor be
86	11	50.0	6	2	PT0718	T-cell receptor be
87	11	50.0	6	2	PT0718	T-cell receptor be
88	11	50.0	6	2	PT0727	T-cell receptor be
89	11	50.0	7	2	PT0246	Ig heavy chain CRD
90	11	50.0	7	2	A11483	aspartate transami
91	11	50.0	7	2	PT0663	T-cell receptor be
92	11	50.0	7	2	T09512	NADH dehydrogenas
93	11	50.0	7	2	PT0529	T-cell receptor be
94	11	50.0	7	4	PC2056	trichodecetin I -
95	11	50.0	7	4	PC2057	trichodecetin II -
96	11	50.0	8	2	PT0368	Ig gamma chain C r
97	11	50.0	8	2	PH1618	Ig H chain V-D-J r
98	11	50.0	8	2	PT0627	T-cell receptor be
99	11	50.0	8	2	PT0522	T-cell receptor be
100	11	50.0	8	2	PT0559	T-cell receptor be
101	11	50.0	8	2	PT0554	T-cell receptor be
102	11	50.0	8	2	PT0725	T-cell receptor be

103	11	50.0	8	2	D47393	neuropeptide calla
104	11	50.0	8	4	I55411	hypothetical hsto
105	11	50.0	9	2	A61230	caldesmonin, cat
106	11	50.0	9	2	S65865	collagen alpha 2(V)
107	11	50.0	9	2	PH1591	ig H chain V-D-J r
108	11	50.0	9	2	PS0253	glycine cleavage s
109	11	50.0	9	2	A60356	118k stomach cance
110	11	50.0	10	1	RHPSG	gonadoliberin - pi
111	11	50.0	10	1	RHSHG	gonadoliberin - bh
112	11	50.0	10	1	RHAOL	gonadoliberin I -
113	11	50.0	10	2	PN0136	pepsin (EC 3.4.23.
114	11	50.0	10	2	C45474	chromospondin 2 -
115	11	50.0	10	2	A35556	hypothetical prote
116	11	50.0	10	2	PH1633	ig H chain V-D-J r
117	11	50.0	10	2	PT0632	T-cell receptor be
118	11	50.0	10	2	PT0664	T-cell receptor be
119	11	50.0	10	2	S43630	cytochrome-c oxida
120	11	50.0	10	2	F60527	sperm-activating p
121	11	50.0	10	2	B60589	sperm-activating p
122	11	50.0	11	2	B58501	bradykinin-potentl
123	11	50.0	11	2	XASNBA	24k kidney and bla
124	11	50.0	11	2	S70720	trigger factor hom
125	11	50.0	11	2	PH1630	ig H chain V-D-J r
126	11	50.0	11	2	PH0939	T-cell receptor be
127	11	50.0	11	2	S19775	wound-induced prot
128	11	50.0	11	2	H84082	hypothetical prote
129	10	45.5	4	2	A53284	T-cell receptor be
130	10	45.5	6	2	B56979	collagen alpha 1(I
131	10	45.5	6	2	A41946	T-cell receptor ga
132	10	45.5	7	2	S68004	hucolin, 75k chain
133	10	45.5	7	2	S09066	globulin IV alpha
134	10	45.5	8	2	S63493	disintegrin-like
135	10	45.5	8	2	PA0032	protein QAJ0040 -
136	10	45.5	9	2	S70332	endospem protein,
137	10	45.5	9	2	S70334	endospem protein,
138	10	45.5	9	2	B33098	231k exoantigen
139	10	45.5	9	2	PT0285	1g heavy chain CRD
140	10	45.5	9	2	PT0670	T-cell receptor be
141	10	45.5	9	2	A56029	N-methylpurine DNA
142	10	45.5	9	2	PC7074	translational elonga
143	10	45.5	10	1	A61126	gonadoliberin - ap
144	10	45.5	10	1	RHA02	gonadoliberin II -
145	10	45.5	10	2	S10926	inhibin beta-A cha
146	10	45.5	10	2	B46030	gonadoliberin II -
147	10	45.5	10	2	C38925	seed storage prote
148	10	45.5	10	2	B24736	inhibin beta-B cha
149	10	45.5	10	2	I48778	small nuclear ribo
150	10	45.5	10	2	D37397	hypothetical prote

## ALIGNMENTS

RESULT 1  
SPPGNK  
neuromedin K - pig  
C:/Species: Sus scrofa domestica (domestic pig)  
C:/Date: 19-Feb-1984 #sequence\_revision 19-Feb-1984 #text\_change 09-Jul-2004  
C:/Accession: A01560  
R:/Kangawa, K.; Minamino, N.; Fukuda, A.; Matsuo, H.  
Biochem. Biophys. Res. Commun. 114, 533-540, 1983  
A:/Title: Neuromedin K: a novel mammalian tachykinin identified in porcine spinal cord.  
A:/Reference number: A01560; PMID:83282812; PMID:6576785  
A:/Accession: A01560  
A:/Molecule type: protein  
A:/Residues: 1-10 <KAN>  
A:/Cross-references: UNIPROT:P01292  
A:/Note: The structure of the peptide was confirmed by synthesis  
C:/Comment: The biological source of this peptide is spinal cord. It stimulates smooth mu  
C:/Superfamily: neurokinin B precursor  
C:/Keywords: amidated carboxyl end; hormone; spinal cord  
F:/10/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 100.0%; Score 22; DB 1; Length 10;  
Best Local Similarity 80.0%; Pred. No. 21;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 FXGLM 5  
Db 6 FVGLM 10

RESULT 2  
JN0024  
neurokinin A - chicken  
C:/Species: Gallus gallus (chicken)  
C:/Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 09-Jul-2004  
C:/Accession: JN0024  
R:/Conlon, J.M.; Katsoulis, S.; Schmidt, W.E.; Thim, L.  
Regul. Pept. 20, 171-180, 1988  
A:/Title: [Arg3]substance P and neurokinin A from chicken small intestine.  
A:/Reference number: JN0023; PMID:8204263; PMID:2452461  
A:/Accession: JN0024  
A:/Molecule type: protein  
A:/Residues: 1-10 <CON>  
A:/Cross-references: UNIPROT:P19851  
C:/Superfamily: substance P precursor  
C:/Keywords: amidated carboxyl end; neuropeptide; tachykinin  
F:/10/Modified site: amidated carboxyl end (Met) #status predicted

Query Match 100.0%; Score 22; DB 2; Length 10;  
Best Local Similarity 80.0%; Pred. No. 21;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 FXGLM 5  
Db 6 FVGLM 10

RESULT 3  
B49581  
sialokinin II - yellow fever mosquito  
C:/Species: Aedes aegypti (yellow fever mosquito)  
C:/Date: 06-Oct-1994 #sequence\_revision 18-Nov-1994 #text\_change 16-Aug-2004  
C:/Accession: B49581  
R:/Champagne, D.E.; Ribeiro, J.M.  
Proc. Natl. Acad. Sci. U.S.A. 91, 138-142, 1994  
A:/Title: Sialokinin I and II: vasodilatory tachykinins from the yellow fever mosquito Aec  
A:/Reference number: A49581; PMID:94105119; PMID:8278354  
A:/Accession: B49581  
A:/Status: preliminary  
A:/Molecule type: protein  
A:/Residues: 1-10 <CHA>  
A:/Cross-references: UNIPROT:P42635  
A:/Experimental source: Rockefeller  
A:/Note: sequence extracted from NCBI backbone (NCBIP:141842)

Query Match 100.0%; Score 22; DB 2; Length 10;  
Best Local Similarity 80.0%; Pred. No. 21;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 FXGLM 5  
Db 6 FVGLM 10

RESULT 4  
A49581  
sialokinin I - yellow fever mosquito  
C:/Species: Aedes aegypti (yellow fever mosquito)  
C:/Date: 06-Oct-1994 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004  
C:/Accession: A49581  
R:/Champagne, D.E.; Ribeiro, J.M.  
Proc. Natl. Acad. Sci. U.S.A. 91, 138-142, 1994  
A:/Title: Sialokinin I and II: vasodilatory tachykinins from the yellow fever mosquito Aec  
A:/Reference number: A49581; PMID:94105119; PMID:8278354

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OM protein - protein search, using sw model

Run on: October 26, 2005, 08:31:09 ; Search time 162 Seconds  
(without alignments)  
12.886 Million cell updates/sec

Title: US-10-053-669-4  
Perfect score: 22  
Sequence: 1 FXGLM 5

Scoring table: BLOSUM62DX  
Gapop 10.0 , Gapext 0.5

Searched: 1862994 seqs, 417510619 residues

Total number of hits satisfying chosen parameters: 250346

Minimum DB seq length: 0  
Maximum DB seq length: 11

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 150 summaries

Database :

Published Applications AA:\*

- 1: /cgn2\_6/prodata/1/pubppaa/US07\_PUBCOMB.pep:\*
- 2: /cgn2\_6/prodata/1/pubppaa/PCT\_NEW\_PUB.pep:\*
- 3: /cgn2\_6/prodata/1/pubppaa/US06\_NEW\_PUB.pep:\*
- 4: /cgn2\_6/prodata/1/pubppaa/US07\_NEW\_PUB.pep:\*
- 5: /cgn2\_6/prodata/1/pubppaa/US06\_PUBCOMB.pep:\*
- 6: /cgn2\_6/prodata/1/pubppaa/PCTUS\_PUBCOMB.pep:\*
- 7: /cgn2\_6/prodata/1/pubppaa/US08\_NEW\_PUB.pep:\*
- 8: /cgn2\_6/prodata/1/pubppaa/US08\_PUBCOMB.pep:\*
- 9: /cgn2\_6/prodata/1/pubppaa/US09\_PUBCOMB.pep:\*
- 10: /cgn2\_6/prodata/1/pubppaa/US09\_PUBCOMB.pep:\*
- 11: /cgn2\_6/prodata/1/pubppaa/US09C\_PUBCOMB.pep:\*
- 12: /cgn2\_6/prodata/1/pubppaa/US09\_NEW\_PUB.pep:\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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6	22	100.0	5 15 US-10-134-187-3	Sequence 3, App1
7	22	100.0	5 16 US-10-688-741-3	Sequence 3, App1
8	22	100.0	5 16 US-10-695-536-4	Sequence 4, App1
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15	22	100.0	5 20 US-11-066-697-604	Sequence 604, App
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; APPLICANT: Wellb, Ibert
; TITLE OF INVENTION: Method for Detecting Deficient Cellular Membrane Tightly Bound Mac
; FILE REFERENCE: 1427001
; CURRENT APPLICATION NUMBER: US/09/265,690C
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (5)..(5)
; OTHER INFORMATION: AMIDATION
US-09-265-690C-1

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Best Local Similarity 80.0%; Pred.No.1.7e+06;
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Db      1 FXGLM 5

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; Sequence 4, Application US/09265690C
; Publication No. US20010051345A1
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; APPLICANT: Wellb, Ibert
; TITLE OF INVENTION: Method for Detecting Deficient Cellular Membrane Tightly Bound Mac
; FILE REFERENCE: 1427001
; CURRENT APPLICATION NUMBER: US/09/265,690C
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: MOD_RES
; LOCATION: (5)..(5)
; OTHER INFORMATION: AMIDATION
; NAME/KEY: VARIANT
; LOCATION: (2)..(2)
; OTHER INFORMATION: "X" may be either Phe or Val.
US-09-265-690C-4

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Query Match          100.0%; Score 22; DB 9; Length 5;
Best Local Similarity 100.0%; Pred.No.1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 FXGLM 5
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Db      1 FXGLM 5

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; Sequence 4, Application US/10230133
; Publication No. US20030040625A1
; GENERAL INFORMATION:
; APPLICANT: Wellb, Ibert
; TITLE OF INVENTION: Antagonists of the magnesium binding defect as therapy agents and
; methods for treatment of abnormal physiological states

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GenCore version 5.1.6  
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OM protein - protein search, using SW model

Run on: October 26, 2005, 08:30:04 ; Search time 21 Seconds  
(without alignments)  
17.774 Million cell updates/sec

Title: US-10-053-669-4  
Perfect score: 22  
Sequence: 1 FXGLM 5

Scoring table: BLOSUM62DX  
Gapop 10.0 Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 125705

Minimum DB seq length: 0  
Maximum DB-seq length: 11

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 150 summaries

Database:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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80	22	100.0	10	4 US-08-153-847-3	Sequence 3, Appli
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82	22	100.0	10	4 US-09-152-060-110	Sequence 110, App
83	22	100.0	10	6 5169865-11	Patent No. 5169865
84	22	100.0	10	6 5169865-11	Patent No. 5169865
85	22	100.0	11	1 US-07-899-205-1	Sequence 1, Appli
86	22	100.0	11	1 US-07-753-909B-2	Sequence 2, Appli
87	22	100.0	11	1 US-07-934-553-1	Sequence 1, Appli
88	22	100.0	11	1 US-08-184-593-12	Sequence 12, Appli
89	22	100.0	11	1 US-08-391-910-2	Sequence 2, Appli
90	22	100.0	11	1 US-08-269-288-2	Sequence 2, Appli
91	22	100.0	11	1 US-08-338-484-1	Sequence 1, Appli
92	22	100.0	11	1 US-08-175-432-1	Sequence 1, Appli
93	22	100.0	11	1 US-08-462-413-2	Sequence 2, Appli
94	22	100.0	11	1 US-08-225-474-1	Sequence 1, Appli
95	22	100.0	11	1 US-08-391-910-2	Sequence 2, Appli
96	22	100.0	11	1 US-08-418-994-2	Sequence 2, Appli
97	22	100.0	11	1 US-08-480-505-3	Sequence 3, Appli
98	22	100.0	11	1 US-08-391-814-2	Sequence 2, Appli
99	22	100.0	11	1 US-08-167-870-1	Sequence 1, Appli
100	22	100.0	11	1 US-08-428-488-15	Sequence 15, Appli
					Sequence 16, Appli

101	22	100.0	11	1	US-08-428-488-17	Sequence 17, Appl
102	22	100.0	11	1	US-08-255-272-6	Sequence 6, Appl1
103	22	100.0	11	1	US-08-441-591-6	Sequence 6, Appl1
104	22	100.0	11	1	US-08-303-362A-6	Sequence 6, Appl1
105	22	100.0	11	1	US-08-462-859A-1	Sequence 1, Appl1
106	22	100.0	11	1	US-08-123-659A-1	Sequence 1, Appl1
107	22	100.0	11	1	US-08-462-415-2	Sequence 2, Appl1
108	22	100.0	11	1	US-08-463-874-2	Sequence 2, Appl1
109	22	100.0	11	1	US-08-464-247A-1	Sequence 1, Appl1
110	22	100.0	11	1	US-08-464-248A-1	Sequence 1, Appl1
111	22	100.0	11	1	US-08-444-135-2	Sequence 2, Appl1
112	22	100.0	11	1	US-08-318-391-2	Sequence 2, Appl1
113	22	100.0	11	2	US-08-796-598-7	Sequence 7, Appl1
114	22	100.0	11	2	US-08-796-598-11	Sequence 11, Appl1
115	22	100.0	11	2	US-08-496-118-1	Sequence 7, Appl1
116	22	100.0	11	2	US-08-447-175A-7	Sequence 11, Appl1
117	22	100.0	11	2	US-08-447-175A-11	Sequence 15, Appl1
118	22	100.0	11	2	US-07-737-311E-15	Sequence 16, Appl1
119	22	100.0	11	2	US-07-737-311E-16	Sequence 18, Appl1
120	22	100.0	11	2	US-07-737-311E-18	Sequence 19, Appl1
121	22	100.0	11	2	US-07-737-311E-19	Sequence 25, Appl1
122	22	100.0	11	2	US-07-737-311E-25	Sequence 26, Appl1
123	22	100.0	11	2	US-07-737-311E-26	Sequence 33, Appl1
124	22	100.0	11	2	US-07-737-311E-33	Sequence 35, Appl1
125	22	100.0	11	2	US-07-737-311E-35	Sequence 36, Appl1
126	22	100.0	11	2	US-07-737-311E-37	Sequence 37, Appl1
127	22	100.0	11	2	US-07-737-311E-38	Sequence 38, Appl1
128	22	100.0	11	2	US-07-737-311E-38	Sequence 77, Appl1
129	22	100.0	11	2	US-07-737-311E-77	Sequence 1, Appl1
130	22	100.0	11	2	US-08-848-766A-1	Sequence 4, Appl1
131	22	100.0	11	3	US-08-850-157A-4	Sequence 17, Appl1
132	22	100.0	11	3	US-08-927-128-17	Sequence 2, Appl1
133	22	100.0	11	3	US-08-257-966-2	Sequence 1, Appl1
134	22	100.0	11	3	US-09-214-614-1	Sequence 3, Appl1
135	22	100.0	11	3	US-09-265-690C-3	Sequence 2, Appl1
136	22	100.0	11	3	US-08-153-847-2	Sequence 1, Appl1
137	22	100.0	11	4	US-09-635-266-1	Sequence 1, Appl1
138	22	100.0	11	4	US-09-570-022-1	Sequence 5, Appl1
139	22	100.0	11	4	US-09-570-022-5	Sequence 6, Appl1
140	22	100.0	11	4	US-09-570-022-6	Sequence 7, Appl1
141	22	100.0	11	4	US-09-570-022-7	Sequence 8, Appl1
142	22	100.0	11	4	US-09-570-022-8	Sequence 9, Appl1
143	22	100.0	11	4	US-09-570-022-9	Sequence 10, Appl1
144	22	100.0	11	4	US-10-002-593-4	Sequence 1, Appl1
145	22	100.0	11	4	US-09-629-642A-1	Sequence 1, Appl1
146	22	100.0	11	4	US-10-230-133-1	Sequence 21, Appl1
147	22	100.0	11	4	US-09-428-692-21	Sequence 1, Appl1
148	22	100.0	11	4	US-09-285-387A-1	Sequence 1, Appl1
149	22	100.0	11	4		
150	22	100.0	11	4		

## ALIGNMENTS

RESULT 1  
US-07-753-909B-3  
Sequence 3, Application US/07753909B  
Patent No. 5304632  
GENERAL INFORMATION:  
APPLICANT: Vaudry, Hubert  
APPLICANT: Conlon, Michael J.  
TITLE OF INVENTION: Neuropeptides of the Tachykinin Family  
NUMBER OF SEQUENCES: 3  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Zarley, McKee, Thomte, Voorhees, and Sease  
STREET: 801 Grand, Suite 3200  
CITY: Des Moines  
STATE: Iowa  
COUNTRY: United States  
ZIP: 50309  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/753,909B  
FILING DATE: 19910903  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: FR 9106759  
FILING DATE: 04-JUN-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Sease, Edmund J.  
REGISTRATION NUMBER: 24,741  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (515)-288-3667  
TELEFAX: (515)-288-1338  
INFORMATION FOR SEQ. ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 amino acids  
TYPE: AMINO ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: C-terminal  
ORIGINAL SOURCE:  
ORGANISM: Rana ridibunda  
DEVELOPMENTAL STAGE: adult  
TISSUE TYPE: brain  
US-07-753-909B-3

Query Match 100.0%; Score 22; DB 1; Length 5;  
Best Local Similarity 100.0%; Pred. No. 4.1e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXGLM 5  
Db 1 FXGLM 5

RESULT 2  
US-07-934-553-2  
Sequence 2, Application US/07934553  
Patent No. 5314690  
GENERAL INFORMATION:  
APPLICANT: PATTERSON, ROY  
APPLICANT: HARRIS, KATHLEEN E  
TITLE OF INVENTION: METHOD AND COMPOSITION FOR REDUCING IGB  
NUMBER OF SEQUENCES: 5  
TITLE OF INVENTION: ANTIBODIES TO SPECIFIC ALLERGENS  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: TILTON, FALLOU, LUNGWUS & CHESTNUT  
STREET: 100 SOUTH WACKER DRIVE  
CITY: CHICAGO  
STATE: ILLINOIS  
COUNTRY: USA  
ZIP: 60606-4002  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/934,553  
FILING DATE: 19920821  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/705,071  
FILING DATE: 24-MAY-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: FENTRESS, SUSAN B  
REGISTRATION NUMBER: 31,327  
REFERENCE/DOCKET NUMBER: NU-9033CIP  
TELECOMMUNICATION INFORMATION:

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 26, 2005, 08:21:45 : Search time 162 Seconds  
(without alignments)  
11.937 Million cell updates/sec

Title: US-10-053-669-4  
Perfect score: 22  
Sequence: 1 FXGLM 5

Scoring table: BLASTN62DX  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 494136

Minimum DB seq length: 0  
Maximum DB seq length: 11

Post-processing: Minimum Match 0%  
Listing first 150 summaries

Database: us-10-053-669-4  
1: Genesegp16Dec04:\*  
2: Genesegp19808:\*  
3: Genesegp20008:\*  
4: Genesegp20018:\*  
5: Genesegp20028:\*  
6: Genesegp20038:\*  
7: Genesegp20038:\*  
8: Genesegp20048:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query	Length	ID	Description
1	22	100.0	5	AAR33009	Aar33009 Alpha-sub
2	22	100.0	5	AAR33008	Aar33008 Alpha-sub
3	22	100.0	5	AAR33007	Aar33007 Alpha-sub
4	22	100.0	5	AAR33010	Aar33010 Alpha-sub
5	22	100.0	5	AAW80134	Aaw80134 COOH-term
6	22	100.0	5	AAW54549	Aaw54549 Cholecyt
7	22	100.0	5	AAW54551	Aaw54551 Cholecyt
8	22	100.0	5	AAW54550	Aaw54550 Cholecyt
9	22	100.0	5	AAW54548	Aaw54548 Cholecyt
10	22	100.0	5	AAW41687	Aaw41687 Tetrapt
11	22	100.0	5	AAW96643	Aaw96643 Substance
12	22	100.0	5	AAW50325	Aaw50325 Neutroph
13	22	100.0	5	AAW92660	Aaw92660 Human tac
14	22	100.0	5	AAW23028	Aab23028 Mammalian
15	22	100.0	5	AAW23025	Aab23025 Human/tac
16	22	100.0	5	AAW67576	Aay67576 P antgon
17	22	100.0	5	AAW66674	Aab66674 C-term
18	22	100.0	5	AAW82430	Aab82430 Fluorinat
19	22	100.0	5	AAW82431	Aab82431 Fluorinat
20	22	100.0	5	AAW81428	Aab81428 Tachykini
21	22	100.0	5	AAW70556	Aab70556 Octopus c
22	22	100.0	5	AAW10880	Aab10880 Human bet
23	22	100.0	5	AAW10088	Aab10088 Substance
24	22	100.0	5	AAW77847	Aau77847 Tachykini
25	22	100.0	5	AAW77845	Aau77845 Tachykini

26	22	100.0	5	ADC64000	Adc64000 Tachykini
27	22	100.0	5	ADBE94203	Adbe94203 High acti
28	22	100.0	5	ADFP2530	Adfp2530 Substance
29	22	100.0	5	ADN12180	Adn12180 Tachykini
30	22	100.0	5	ADN95078	Adn95078 Mammalian
31	22	100.0	5	ADN43774	Adn43774 Mammalian
32	22	100.0	5	ADN43771	Adn43771 Human mag
33	22	100.0	6	ADP30443	Adp30443 Sequence
34	22	100.0	6	ADP40519	Adp40519 Sequence
35	22	100.0	6	ADP50694	Adp50694 Sequence
36	22	100.0	6	ADP50632	Adp50632 Substance
37	22	100.0	6	ADP61486	Adp61486 Peptide h
38	22	100.0	6	ADP07897	Adp07897 Cylopept
39	22	100.0	6	ADP07893	Adp07893 Cylopept
40	22	100.0	6	ADP21959	Adp21959 Substance
41	22	100.0	6	ADP27696	Adp27696 Cyclic ta
42	22	100.0	6	ADP27694	Adp27694 Cyclic ta
43	22	100.0	6	ADP27695	Adp27695 Cyclic ta
44	22	100.0	6	ADP9686	Adp9686 Substance
45	22	100.0	6	ADP92706	Adp92706 Human tac
46	22	100.0	6	ADP92659	Adp92659 Human tac
47	22	100.0	6	ADP31052	Adp31052 Non-cross
48	22	100.0	6	ADP67575	Adp67575 P antgon
49	22	100.0	6	ADP82453	Adp82453 Fluorinat
50	22	100.0	6	ADP82432	Adp82432 Fluorinat
51	22	100.0	6	ADP82436	Adp82436 Fluorinat
52	22	100.0	6	ADP82433	Adp82433 Fluorinat
53	22	100.0	6	ADP81421	Adp81421 Tachykini
54	22	100.0	6	ADP81425	Adp81425 Tachykini
55	22	100.0	6	ADP81419	Adp81419 Tachykini
56	22	100.0	6	ADP93351	Adp93351 Aclypical
57	22	100.0	6	ADP74306	Adp74306 Peptide a
58	22	100.0	6	ADP89884	Adp89884 Chimeric
59	22	100.0	6	ADP89886	Adp89886 Chimeric
60	22	100.0	6	ADP10087	Adp10087 Substance
61	22	100.0	6	ADP10086	Adp10086 Substance
62	22	100.0	6	ADP37288	Adp37288 Rhodopsin
63	22	100.0	6	ADP94202	Adp94202 High acti
64	22	100.0	7	ADP20310	Adp20310 Tyr8-SP5-
65	22	100.0	7	ADP21956	Adp21956 Substance
66	22	100.0	7	ADP21957	Adp21957 Substance
67	22	100.0	7	ADP29539	Adp29539 Asp-Ser-P
68	22	100.0	7	ADP50324	Adp50324 Neutroph
69	22	100.0	7	ADP2662	Adp2662 Human tac
70	22	100.0	7	ADP92705	Adp92705 Human tac
71	22	100.0	7	ADP67574	Adp67574 P antgon
72	22	100.0	7	ADP80323	Adp80323 Human pro
73	22	100.0	7	ADP80324	Adp80324 Human pro
74	22	100.0	7	ADP82428	Adp82428 Fluorinat
75	22	100.0	7	ADP82429	Adp82429 Fluorinat
76	22	100.0	7	ADP81354	Adp81354 Tachykini
77	22	100.0	7	ADP81431	Adp81431 Tachykini
78	22	100.0	7	ADP81420	Adp81420 Tachykini
79	22	100.0	7	ADP93350	Adp93350 Aclypical
80	22	100.0	7	ADP89845	Adp89845 Chimeric
81	22	100.0	7	ADP810085	Adp810085 Substance
82	22	100.0	7	ADP09500	Adp09500 Substance
83	22	100.0	7	ADP94201	Adp94201 High acti
84	22	100.0	7	ADP92529	Adp92529 Substance
85	22	100.0	7	ADP95077	Adp95077 Mammalian
86	22	100.0	8	ADP20303	Adp20303 Gastroint
87	22	100.0	8	ADP28444	Adp28444 Neurokin
88	22	100.0	8	ADP57536	Adp57536 Molecular
89	22	100.0	8	ADP2664	Adp2664 Human tac
90	22	100.0	8	ADP92710	Adp92710 Human tac
91	22	100.0	8	ADP67573	Adp67573 P antgon
92	22	100.0	8	ADP81407	Adp81407 Tachykini
93	22	100.0	8	ADP81416	Adp81416 Tachykini
94	22	100.0	8	ADP81424	Adp81424 Tachykini
95	22	100.0	8	ADP93349	Adp93349 Atypical
96	22	100.0	8	ADP97571	Adp97571 Substicuc
97	22	100.0	8	ADP09498	Adp09498 Substance
98	22	100.0	8	ADP09499	Adp09499 Substance

99	22	100.0	8	7	ADB94200	AdB94200 High acti
100	22	100.0	9	1	AAp50634	AAp50634 Substance
101	22	100.0	9	2	AAW92714	AAW92714 Human tac
102	22	100.0	9	4	AAAB80325	AAAB80325 Human pro
103	22	100.0	9	4	AAAB91446	AAAB91446 Tachykini
104	22	100.0	9	4	AAAB91369	AAAB91369 Tachykini
105	22	100.0	9	4	AAAG99348	AAAG99348 Atypical
106	22	100.0	9	7	ADP92528	ADP92528 Substance
107	22	100.0	9	8	ADN95076	ADN95076 Mammalian
108	22	100.0	10	1	AAp40414	AAp40414 Decapepti
109	22	100.0	10	1	AAp50633	AAp50633 Substance
110	22	100.0	10	2	AAAB21933	AAAB21933 Substance
111	22	100.0	10	2	AAAB5181	AAAB5181 S. cerevi
112	22	100.0	10	2	AAAB77311	AAAB77311 Neurokini
113	22	100.0	10	2	AAAB77312	AAAB77312 Neurokini
114	22	100.0	10	2	AAAB77776	AAAB77776 Neurokini
115	22	100.0	10	2	AAAB79776	AAAB79776 Neurokini
116	22	100.0	10	2	AAAB8951	AAAB8951 Tachykini
117	22	100.0	10	2	AAAB8951	AAAB8951 Tachykini
118	22	100.0	10	2	AAAB8951	AAAB8951 Tachykini
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125	22	100.0	10	2	AAAB8951	AAAB8951 Tachykini
126	22	100.0	10	2	AAAB8951	AAAB8951 Tachykini
127	22	100.0	10	2	AAAB8951	AAAB8951 Tachykini
128	22	100.0	10	2	AAAB8951	AAAB8951 Tachykini
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137	22	100.0	10	2	AAAB8951	AAAB8951 Tachykini
138	22	100.0	10	2	AAAB8951	AAAB8951 Tachykini
139	22	100.0	10	2	AAAB8951	AAAB8951 Tachykini
140	22	100.0	10	2	AAAB8951	AAAB8951 Tachykini
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142	22	100.0	10	2	AAAB8951	AAAB8951 Tachykini
143	22	100.0	10	2	AAAB8951	AAAB8951 Tachykini
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146	22	100.0	10	2	AAAB8951	AAAB8951 Tachykini
147	22	100.0	10	2	AAAB8951	AAAB8951 Tachykini
148	22	100.0	10	2	AAAB8951	AAAB8951 Tachykini
149	22	100.0	10	2	AAAB8951	AAAB8951 Tachykini
150	22	100.0	10	2	AAAB8951	AAAB8951 Tachykini

## ALIGNMENTS

RESULT 1  
AAR33009 standard; peptide; 5 AA.  
ID AAR33009;  
AC AAR33009;  
XX 25-MAR-2003 (revised)  
DT 02-APR-1993 (first entry)  
XX Alpha-substituted short peptide.  
XX CCK; neuropeptide; endorphin; hormone; LHRH; contraception; analgesia;  
XX Improved bioavailability.  
XX Synthetic.

PH Key Location/Qualifiers  
FT Modified-site 4  
FT Modified-site /note= "alpha-Me-Leu"  
FT Modified-site 5  
FT Modified-site /note= "Met-NH2"  
XX MO9219254-A1.  
XX 12-NOV-1992.  
XX 15-APR-1992; 92MO-US003119.  
XX 24-APR-1991; 91US-00690755.  
XX 20-MAR-1992; 92US-00852086.  
XX (WARN ) WARNER LAMBERT CO.  
XX Horwell DC, Hughes J, Richardson RS, Howson W;  
XX WPI; 1992-398522/48.  
XX New alpha-subst. polypeptide are e.g. selective receptor ligands - for  
XX treating inflammation, pain, stroke, ulcers, hypertension, heart failure,  
XX depression, cancer, asthma, psychosis, arthritis, etc.  
XX Claim 3; Page 41; 46pp; English.  
XX The peptide is a specifically claimed example of a group of generically  
XX claimed mono-, di-, tri-, tetra- and penta-peptides which include a  
XX substituent on an alpha-C atom in the chain. Such substitution may modify  
XX the bioavailability, stability or absorbability of the peptide and hence  
XX nature of the parent peptide (hormone, endorphin, CCK, NK2, chemotactic  
XX peptide, etc.), the modified peptides are variously useful for treating  
XX obesity, anxiety, gastrointestinal ulcers, pain, stroke, inflammation,  
XX addictive drug withdrawal symptoms, hypertension, heart failure,  
XX cognition or memory disorders, spasticity, depression, diabetes, cancer,  
XX asthma, bladder dysfunction, psychosis and arthritis; and as  
XX contraceptives. (Updated on 25-MAR-2003 to correct PN field.) (Updated on  
XX 25-MAR-2003 to correct PD field.) (Updated on 25-MAR-2003 to correct PR  
XX field.) (Updated on 25-MAR-2003 to correct PI field.)  
SQ Sequence 5 AA;  
QY Query Match 100.0%; Score 22; DB 2; Length 5;  
DB Best Local Similarity 80.0%; Pred. No. 1.8e+06;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
1 FYGLM 5  
1 FYGLM 5  
RESULT 2  
AAR33008  
ID AAR33008 standard; peptide; 5 AA.  
XX AAR33008;  
XX 25-MAR-2003 (revised)  
DT 02-APR-1993 (first entry)  
XX Alpha-substituted short peptide.  
XX CCK; neuropeptide; endorphin; hormone; LHRH; contraception; analgesia;  
XX Improved bioavailability.  
XX Synthetic.  
XX Key Location/Qualifiers  
FT Modified-site 2  
FT Modified-site /note= "alpha-Me-Phe"  
FT Modified-site 5